

18561
SEARCH REQUEST FORM

Examiner # (Mandatory): _____ Requester's Full Name: _____

Art Unit _____ Location (Bldg/Room#): _____ Phone (circle 305 306 308) _____

Serial Number: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Date: _____

Keywords (include any known synonyms registry numbers, explanation of initialisms): _____

Search Topic:

Please write detailed statement of the search topic, and the concept of the invention. Describe as specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples of relevant citations, authors, etc., if known. You may include a copy of the abstract and the broadcast or most relevant claim(s).

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STAFF USE ONLYSearcher: JanSearcher Phone #: 4498

Searcher Location: _____

Date Picked Up: 8/21/99Date Completed: 8/23/99Clerical Prep Time: 60 / 90Terminal Time: 30 / 90Number of Databases: 11

Type of Search _____ Vendors (include cost where applicable)

☒ N.A. Sequence X4 _____ STN☒ A.A. Sequence X10 _____ Questel/Orbit

_____ Structure (#) _____ Lexis/Nexis

_____ Bibliographic _____ WWW/Internet

_____ Litigation1 ☒ In-house sequence systems (list)

_____ Fulltext _____ Dialog

_____ Procurement _____ Dr. Link

_____ Other _____ Westlaw

_____ Other (specify)

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 M P S E R I F
 (7M)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm
 Run on: Sat Aug 21 12:10:37 1999; Maspar time 18.24 Seconds
 Tabular output not generated. 979.934 Million cell updates/sec

Title: >US-09-219-935-5
 Description: (1-446) from US09219935.pep
 Sequence: 1 MANLVSESGIRPLPRITYT.....EVVYKADPNLGEVVRAD 446

Scoring table: TABLE uniprottable
 Gap 60

Searched: 122810 segs, 40068593 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r60
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 3.698; Variance 0.462; scale 8.000

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|-------------|---------------------------------|
| 1 | 446 | 100.0 | 446 | 2 | J02336 | omega-3 fatty acid de 0.00e+00 |
| 2 | 103 | 23.1 | 404 | 2 | P00812 | omega-3 fatty acid de 1.77e-300 |
| 3 | 43 | 9.6 | 398 | 2 | T01566 | omega-3 fatty acid de 7.85e-103 |
| 4 | 40 | 9.0 | 441 | 2 | T03029 | omega-3 fatty acid de 2.65e-93 |
| 5 | 36 | 8.1 | 443 | 2 | T01697 | omega-3 fatty acid de 1.04e-80 |
| 6 | 36 | 8.1 | 453 | 2 | J02339 | omega-3 fatty acid de 1.04e-80 |
| 7 | 28 | 6.3 | 377 | 2 | J02337 | omega-3 fatty acid de 5.10e-56 |
| 8 | 28 | 6.3 | 383 | 2 | A44227 | omega-3 fatty acid de 5.10e-56 |
| 9 | 28 | 6.3 | 386 | 2 | J02335 | omega-3 fatty acid de 5.10e-56 |
| 10 | 27 | 6.1 | 380 | 2 | J02338 | omega-3 fatty acid de 5.41e-53 |
| 11 | 24 | 5.4 | 359 | 2 | UC2555 | omega-3 fatty acid de 5.04e-44 |
| 12 | 16 | 3.6 | 359 | 2 | S52650 | omega-3 fatty acid de 3.19e-21 |
| 13 | 8 | 1.8 | 429 | 2 | H71349 | probable ribosomal pr 6.82e-02 |
| 14 | 8 | 1.8 | 429 | 2 | S01919 | knirps protein - fruit 6.82e-02 |
| 15 | 8 | 1.8 | 598 | 2 | S65770 | maltooligosyltrehalos 6.82e-02 |
| 16 | 7 | 1.6 | 113 | 2 | A60887 | synuclein - Pacific e 4.99e+00 |
| 17 | 7 | 1.6 | 158 | 2 | D71111 | hypothetical protein 4.99e+00 |
| 18 | 7 | 1.6 | 193 | 2 | S67699 | probable membrane pro 4.99e+00 |
| 19 | 7 | 1.6 | 212 | 2 | F71182 | hypothetical protein 4.99e+00 |
| 20 | 7 | 1.6 | 213 | 2 | S08313 | abscisic acid-induced 4.99e+00 |
| 21 | 7 | 1.6 | 257 | 2 | D70341 | hypothetical protein 4.99e+00 |
| 22 | 7 | 1.6 | 257 | 2 | S16865 | gene f41 protein - mo 4.99e+00 |
| 23 | 7 | 1.6 | 305 | 2 | A70212 | conserved hypothetical 4.99e+00 |

| 24 | 7 | 1.6 | 326 | 2 | S34427 | tristetrapoline prot 4.99e+00 |
|----|---|-----|------|---|--------|---------------------------------|
| 25 | 7 | 1.6 | 329 | 1 | VGXRC2 | glucoprotein VP7 prec 4.99e+00 |
| 26 | 7 | 1.6 | 332 | 2 | A57140 | mcb protein homolog 4.99e+00 |
| 27 | 7 | 1.6 | 337 | 2 | A54214 | pentalenene synthase 4.99e+00 |
| 28 | 7 | 1.6 | 367 | 1 | WOHU | alpha-2-HS-glycoprote 4.99e+00 |
| 29 | 7 | 1.6 | 388 | 1 | S72995 | alanine racemase (PC 4.99e+00 |
| 30 | 7 | 1.6 | 389 | 2 | F69336 | conserved hypothetical 4.99e+00 |
| 31 | 7 | 1.6 | 389 | 2 | D40785 | hypothetical protein, 4.99e+00 |
| 32 | 7 | 1.6 | 415 | 1 | C64473 | adenosylhomocysteinas 4.99e+00 |
| 33 | 7 | 1.6 | 468 | 2 | A64956 | flagellar hook-associ 4.99e+00 |
| 34 | 7 | 1.6 | 481 | 2 | A56346 | transcription factor 4.99e+00 |
| 35 | 7 | 1.6 | 555 | 2 | I51671 | Weela kinase - Africa 4.99e+00 |
| 36 | 7 | 1.6 | 649 | 2 | S67787 | hypothetical protein 4.99e+00 |
| 37 | 7 | 1.6 | 733 | 2 | S78376 | photosystem I protein 4.99e+00 |
| 38 | 7 | 1.6 | 741 | 1 | S20923 | photosystem I protein 4.99e+00 |
| 39 | 7 | 1.6 | 754 | 2 | S61113 | YRA6 protein - Yeast 4.99e+00 |
| 40 | 7 | 1.6 | 790 | 2 | G02678 | cadherin-14 - human 4.99e+00 |
| 41 | 7 | 1.6 | 792 | 2 | S63141 | hypothetical protein 4.99e+00 |
| 42 | 7 | 1.6 | 809 | 2 | A46747 | Na+/H+-exchanging pro 4.99e+00 |
| 43 | 7 | 1.6 | 918 | 2 | S04255 | regulatory protein qa 4.99e+00 |
| 44 | 7 | 1.6 | 1065 | 2 | E69795 | acriflavin resistance 4.99e+00 |
| 45 | 7 | 1.6 | 2038 | 2 | A43742 | female sterile homoot 4.99e+00 |

ALIGNMENTS

| RESULT ENTRY TITLE | 1 | J02336 | #type complete |
|-----------------------|--|---|----------------|
| ORGANISM | omega-3 fatty acid desaturase (EC 1.14.99.-) CPD - Arabidopsis thaliana | | |
| DATE | 30-Sep-1993 | sequence_revision 20-Aug-1994 | #text_change |
| ACCESSIONS | J02335 | A49503 | |
| REFERENCE | #authors | Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J. | |
| | #journal | Plant Physiol. (1993) 103:467-476 | |
| | #title | Cloning of higher plant omega-3 fatty acid desaturases. | |
| | #cross-references | MUID:94302147 | |
| | #accession | J02336 | |
| | #molecule_type | mRNA | |
| | #residues | 1-446 | #label YAD |
| REFERENCE | A49503 | | |
| | #authors | Iba, K.; Gibson, S.; Nishitani, T.; Fuse, T.; Nishimura, M.; Arndel, V.; Hugly, S.; Somerville, C. | |
| | #title | J. Biol. Chem. (1993) 268:24099-24105 | |
| | #journal | A gene encoding a chloroplast omega-3 fatty acid desaturase complements alterations in fatty acid desaturation and chloroplast copy number of the fat7 mutant of Arabidopsis thaliana. | |
| | #cross-references | MUID:94043239 | |
| | #accession | A49503 | |
| | #status | preliminary | |
| | #molecule_type | DNA | |
| | #residues | 1-446 | #label IBA |
| | #cross-references | GB:J04007; MID:9461160; PID:01003612; PID:9541653 | |
| | #note | sequence extracted from NCBI backbone (NCBIN:139485, NCBI:139486) | |
| COMMENT | The omega-6 and omega-3 fatty acid desaturases introduce the second and the third double bonds, respectively, in the biosynthesis of 18:2 and 18:3 fatty acids, which are important constituents of plant membranes. | | |
| CLASSIFICATION | #superfamily omega-3 fatty acid desaturase | | |
| KEYWORDS | oxidoreductase | | |
| SUMMARY | #length 446 #molecular-weight 51174 #checksum 4653 | | |
| Query Match | 100.0%; Score 446; DB 2; Length 446; | | |
| Best Local Similarity | 100.0%; Pred. No. 0.00e+00; | | |

Matches 446: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Db 1 MANLVSECGIRPLEPRITTPRSNFLSNKKFRPSLSSSSYKTSPLSGINSRDGFTTR 60
QY 1 MANLVSECGIRPLEPRITTPRSNFLSNKKFRPSLSSSSYKTSPLSGINSRDGFTTR 60
Db 61 NMALVNSPLTPTRFEESEPLEDNKORFDPGAPPPFNADIRAAIPKHCWKNPKKSLSY 120
QY 61 NMALVNSPLTPTRFEESEPLEDNKORFDPGAPPPFNADIRAAIPKHCWKNPKKSLSY 120
Db 121 VVRDVAIFALAGAAAYLNMMIWMPLYLAAOTGMFALFVLGHDGHSFSDNPKLNSV 180
QY 121 VVRDVAIFALAGAAAYLNMMIWMPLYLAAOTGMFALFVLGHDGHSFSDNPKLNSV 180
Db 181 GHLHSSLLVPRHGWIRISHRTHQNHGVHENDESHVPMSEKIYNTLDRPFRFTPLDY 240
QY 181 GHLHSSLLVPRHGWIRISHRTHQNHGVHENDESHVPMSEKIYNTLDRPFRFTPLDY 240
Db 241 MLAYPFYLMASPGKKGSHYHPDSOLFPRKERKDYLTSTACTMAAALLVCLNTFTGSIQ 300
QY 241 MLAYPFYLMASPGKKGSHYHPDSOLFPRKERKDYLTSTACTMAAALLVCLNTFTGSIQ 300
Db 301 MLKLGIRPYWINVMDLVYTLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
QY 301 MLKLGIRPYWINVMDLVYTLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIH 360
Db 361 HDIGTHVHNLFPQIPHYHLVEATEAKPVLGKYRBDKSGPLRLHLEILAKSIKEDH 420
QY 361 HDIGTHVHNLFPQIPHYHLVEATEAKPVLGKYRBDKSGPLRLHLEILAKSIKEDH 420
Db 421 YVSDGEVYVYKADPNLGEVAVRAD 446
QY 421 YVSDGEVYVYKADPNLGEVAVRAD 446

RESULT 2
ENTRY PQ0812 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
ACCESSION PQ0812
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booch Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession PQ0812
#contents CDNA:BND
#molecule_type mRNA
#residues 1-404 #label YAD
#cross-references GB:L22863
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 23.1%; Score 103; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.77e-300;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 IPYWINVMDLVYTLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTH 324
QY 307 IPYWINVMDLVYTLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNIHHDIGTH 366
Db 325 VHHHFPQIPHYHLVEATEAKPVLGKYRBDKSGPLRLH 367

QY 367 VHHHFPQIPHYHLVEATEAKPVLGKYRBDKSGPLRLH 409

RESULT 3
ENTRY T01696 #type fragment
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize (fragment)
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 19-Feb-1999
ACCESSION T01696
REFERENCE 214400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.
#accession T01696
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label BER
#cross-references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum

GENETICS FAD8
KEYWORDS oxidoreductase
SUMMARY #length 398 #checksum 5580

Query Match 9.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 7.85e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGGLTTLDRDYGILNNIHHDIGTHVHNLFPQIPHYHL 333
QY 338 EMSYLRGGLTTLDRDYGILNNIHHDIGTHVHNLFPQIPHYHL 380

RESULT 4
ENTRY T03029 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common tobacco
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
ACCESSION T03029
REFERENCE Z14828
#authors Hamaeda, T.; Nishinuchi, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Plant Cell Physiol. (1996) 37:606-611
#title CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid desaturase from tobacco.
#accession T03029
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:d1093316; PID:q1694625
#experimental_source cultivar SRI

GENETICS FAD7
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 441 #molecular-weight 50310 #checksum 6941

Query Match 9.0%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 2.65e-93;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNHHHDIGTHVHNLFPQIPHYHLVEATEAKPVLGKY 394
QY 356 INNHHHDIGTHVHNLFPQIPHYHLVEATEAKPVLGKY 395

RESULT 5
ENTRY T01697 #type complete

TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999

ACCESSIONS T01697
REFERENCE Z14400

#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.

#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.

#accession T01697
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 #label BER
#cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantum

GENETICS

KEYWORDS FAD7
#gene 163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3
#introns
#keywords oxidoreductase
SUMMARY #length 443 #molecular_weight 49437 #checksum 8872

Query Match 8.1%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.04e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGHEDKLPWYRGKEMSYLRGLTLDROYG 352
|||
QY 319 VTYLHHGHEDKLPWYRGKEMSYLRGLTLDROYG 354

RESULT 6

ENTRY J02339 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS J02339
REFERENCE J02335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents cDNA:GMD
#accession J02339
#molecule_type mRNA
#residues 1-453 #label YAD
#cross-references GB:L122965; NID:q408791; PID:q408792
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular_weight 51362 #checksum 7549

Query Match 8.1%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.04e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPWYRGKEMSYLRGLTLDROYG 362
|||
QY 319 VTYLHHGHEDKLPWYRGKEMSYLRGLTLDROYG 354

RESULT 7

ENTRY J02337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORGANISM #formal_name Brassica napus #common_name rape

DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS J02337
REFERENCE J02335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents cDNA:BN3
#accession J02337
#molecule_type mRNA
#residues 1-377 #label YAD
#cross-references GB:L122962; NID:q408491; PID:q408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular_weight 43258 #checksum 3294

Query Match 6.3%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVPHGWRISHRTHQNHGVNDESW 144
|||
QY 188 ILVPHGWRISHRTHQNHGVNDESW 215

RESULT 8

ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES omega-3 linoleate desaturase
ORGANISM #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227

#authors Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-383 #label ANO
#cross-references GB:L01418; NID:g167147; PID:g167148
#experimental_source developing seed
#note sequence extracted from NCBI backbone (NCBIP:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular_weight 43936 #checksum 2897

Query Match 6.3%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGWRISHRTHQNHGVNDESW 150
|||
QY 188 ILVPHGWRISHRTHQNHGVNDESW 215

RESULT 9

ENTRY J02335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear

DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
ACCESSIONS J02335; J02487
REFERENCE J02335
#authors Yaday, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02335
#molecule_type mRNA
#residues 1-386 #label YAD
REFERENCE 214675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission Submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F3F1 genomic
sequence.
#accession T02487
#status Translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-386 #label ROU
#cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23F1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 5.3%; Score 28; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 5.10e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPGHGRISHRTGHQNGHVENDESW 153
|||||
QY 188 ILVPGHGRISHRTGHQNGHVENDESW 215

RESULT 10
ENTRY J02338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS J02338
REFERENCE J02338
#authors Yaday, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02338
#molecule_type mRNA
#residues 1-380 #label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659

Query Match 6.1%; Score 27; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.41e-53;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NIHHDIGTHVHHLFQIPHYHLEAT 321
|||||
QY 358 NIHHDIGTHVHHLFQIPHYHLEAT 384

RESULT 11
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references MUID:95011632
#accession JC2555
#status Preliminary
#molecule_type mRNA
#residues 1-379 #label HAM
#cross-references DBJ:J26509; NID:g1311480; PID:d1006059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular-weight 44149 #checksum 1940

Query Match 5.4%; Score 24; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 5.04e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 NIHHDIGTHVHHLFQIPHYHL 314
|||||
QY 357 NIHHDIGTHVHHLFQIPHYHL 380

RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis
ORGANISM #formal_name Synechocystis sp.
ALTERNATE_NAMES delta 15 desaturase
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
ACCESSIONS S52650; S75843
REFERENCE S52650; S75843
#authors Sakamoto, T.; Ios, D.A.; Higashi, S.; Wada, H.; Nishida, I.;
Ohmori, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from Cyanobacteria and its use
in altering the degree of membrane-lipid unsaturation.
#cross-references MUID:95035996
#accession S52650
#molecule_type DNA
#residues 1-359 #label SAK
#cross-references GB:D13780; NID:g600596; PID:d1003430; PID:g600598
#note the authors translated the initiation codon GTG for
residue 1 as Val

REFERENCE S74322
#authors Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugino, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Murai, A.; Nakazaki, N.; Natsu, K.; Okumura, S.; Shimpo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.

#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MWID:97061201
#accession S75843
#status nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-359 #label KAN
#cross-references EMBL:D09913; GB:AB001339; NID:91653348; PID:d1019035; PID:91653388
#note the nucleotide sequence was submitted to the EMBL Data Library, June 1996

GENETICS
#start codon GTG
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 359 #molecular-weight 41919 #checksum 9162

Query Match
Best Local Similarity 100.0%; Pred. No. 3,19e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRISHRTH 129
114 ILVPHGWRISHRTH 203

RESULT 13
ENTRY H71349 #type complete
TITLE probable ribosomal protein L1 (rplA) - syphilis spirochete
ORGANISM #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999

ACCESSIONS
H71349
REFERENCE A71250
#authors Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDonald, L.; Artlich, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

#journal Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
#title Science (1998) 281:375-388
#cross-references MWID:98332770
#accession H71349
#status preliminary; nucleic acid sequence not shown; translation not shown
#molecule-type DNA
#residues 1-226 #label COL
#cross-references GB:AE001205; GB:AE000520; NID:93322501; PID:93322508
#experimental_source strain Nichols

GENETICS
#gene TP0238
CLASSIFICATION #superfamily Escherichia coli ribosomal protein L1
SUMMARY #length 226 #molecular-weight 24977 #checksum 6350

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAAGAY 90
113 ALAAGAY 137

RESULT 14
ENTRY S01919 #type complete

TITLE knirps protein - fruit fly (*Drosophila melanogaster*)
ORGANISM #formal_name *Drosophila melanogaster*
DATE 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Sep-1998
ACCESSIONS S01919; S02057
REFERENCE S01919
#authors Nauber, U.; Pankratz, M.J.; Kienlin, A.; Seifert, E.; Klemm, U.; Jaekle, H.
#journal Nature (1988) 336:489-492
#title Abdominal segmentation of the *Drosophila* embryo requires a hormone receptor-like protein encoded by the gap gene knirps.
#cross-references MWID:89057148
#accession S01919
#molecule-type DNA
#residues 1-429 #label NAU1
REFERENCE S02057
#authors Nauber, U.
#submission submitted to the EMBL Data Library, October 1988
#accession S02057
#molecule-type DNA
#residues 1-106, 'L', 108-429 #label NAU2
#cross-references EMBL:X13331; NID:98153; PID:98154

GENETICS
#gene knirps
#cross-references FlyBase:FBgn0001320
#introns 26/3
KEYWORDS DNA binding; nucleus; transcription regulation; zinc finger
SUMMARY #length 429 #molecular-weight 45585 #checksum 9430

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 288 TSSSPLSF 295
43 TSSSPLSF 50

RESULT 15
ENTRY S65770 #type complete
TITLE maltoligosyltrehalose trehalohydrolase - *Arthrobacter* sp.
ORGANISM #formal_name *Arthrobacter* sp.
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Sep-1998
ACCESSIONS S65770
REFERENCE S65769
#authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto, T.; Kurimoto, M.
#journal Biochim. Biophys. Acta (1996) 1289:10-13
#title Cloning and sequencing of trehalose blosynthesis genes from *Arthrobacter* sp. Q36.
#cross-references MWID:96195835
#accession S65770
#status preliminary
#molecule-type DNA
#residues 1-598 #label MAR
#cross-references EMBL:D63343; NID:91255444; PID:d1010313; PID:91255446

CLASSIFICATION #superfamily trehalose trehalohydrolase
SUMMARY #length 598 #molecular-weight 65831 #checksum 4532

Query Match
Best Local Similarity 100.0%; Pred. No. 6.82e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAKPYVG 15
385 EAKPYVG 392

Mon Aug 23 09:46:21 1999

US-09-219-935-5.rpt

Page 6

Search completed: Sat Aug 21 12:11:46 1999
Job time : 69 secs.

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Run on: Sat Aug 21 12:12:03 1999; Maspar time 12.66 Seconds
Tabular output not generated.

Title: >US-09-219-935-5
Description: (1-446) from US09219935.pep
Perfect Score: 446
Sequence: 1 MANVLSCGIRPLPRITTT.....EVVYKADPNLXGEVYKVRAD 446

Scoring table: TABLE uniprottable
Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 3.773; Variance 0.430; scale 8.776

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 446 | 100.0 | 446 | 1 | FD3C_ARATH OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 2 | 103 | 23.1 | 404 | 1 | FD3C_BRANA OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 3 | 44 | 9.9 | 460 | 1 | FD3C_RICCO OMEGA-3 FATTY ACID DES | 5.10e-116 |
| 4 | 43 | 9.6 | 435 | 1 | FD3D_ARATH TEMPERATURE-SENSITIVE | 1.58e-112 |
| 5 | 36 | 8.1 | 447 | 1 | FD3C_SESIN OMEGA-3 FATTY ACID DES | 2.56e-88 |
| 6 | 36 | 8.1 | 453 | 1 | FD3C_SOYBN OMEGA-3 FATTY ACID DES | 2.56e-88 |
| 7 | 28 | 6.3 | 377 | 1 | FD3J_BRANA OMEGA-3 FATTY ACID DES | 2.56e-61 |
| 8 | 28 | 6.3 | 383 | 1 | FD3J_BRANA OMEGA-3 FATTY ACID DES | 2.56e-61 |
| 9 | 28 | 6.3 | 386 | 1 | FD3E_ARATH OMEGA-3 FATTY ACID DES | 2.56e-61 |
| 10 | 27 | 6.1 | 380 | 1 | FD3E_SOYBN OMEGA-3 FATTY ACID DES | 5.18e-58 |
| 11 | 25 | 5.6 | 380 | 1 | FD3E_PHAU OMEGA-3 FATTY ACID DES | 1.86e-51 |
| 12 | 24 | 5.4 | 379 | 1 | FD3E_TOBAC OMEGA-3 FATTY ACID DES | 3.27e-48 |
| 13 | 8 | 1.8 | 226 | 1 | R1L_TREPA 50S RIBOSOMAL PROTEIN | 2.29e-02 |
| 14 | 8 | 1.8 | 429 | 1 | KNIR_DROME ZIGOTIC GAP PROTEIN KN | 2.29e-02 |
| 15 | 7 | 1.6 | 85 | 1 | SYU_TORCA 50S RIBOSOMAL PROTEIN | 2.28e+00 |
| 16 | 7 | 1.6 | 143 | 1 | SYU_TORCA SYNOCLEIN. | 2.28e+00 |
| 17 | 7 | 1.6 | 172 | 1 | YVT6_YEAST HYPOTHETICAL 19.2 KD P | 2.28e+00 |
| 18 | 7 | 1.6 | 213 | 1 | LEAL_HORVA ABA-INDUCIBLE PROTEIN | 2.28e+00 |
| 19 | 7 | 1.6 | 232 | 1 | Y08E_MYCU HYPOTHETICAL 23.9 KD P | 2.28e+00 |
| 20 | 7 | 1.6 | 257 | 1 | BT41_MOUSE BRAIN PROTEIN F41. | 2.28e+00 |
| 21 | 7 | 1.6 | 326 | 1 | TTP_HUMAN TRISTESTEROLINE (TTP) | 2.28e+00 |
| 22 | 7 | 1.6 | 329 | 1 | VS09_ROTCC GLYCOPROTEIN VP7 (SERO | 2.28e+00 |
| 23 | 7 | 1.6 | 336 | 1 | P1LS_STRSC PENTALENE SYNTHASE (| 2.28e+00 |

| RESULT | 1 | STANDARD: | PRT: | 446 AA. | ALIGNMENTS |
|--------|---|-----------|------|---------|------------|
| ID | FD3C_ARATH | | | | |
| AC | P46310; | | | | |
| DT | 01-NOV-1995 (REL. 32, CREATED) | | | | |
| DT | 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) | | | | |
| DE | OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-). | | | | |
| GN | PNP7 OR FAD7. | | | | |
| OS | ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). | | | | |
| OG | CHLOROPLAST. | | | | |
| OC | EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; | | | | |
| OC | EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; | | | | |
| OC | CAPRALES; BRASSICACEAE; ARABIDOPSIS. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL; | | | | |
| RX | MEDLINE; 94032147. | | | | |
| RA | YDAN N.S., WIERZBICKI A., AEGERTER M., GASTER C.S., PEREZ-GRAU L., | | | | |
| RA | KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWENGER B., STECCA K.L., | | | | |
| RA | ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H., | | | | |
| RA | FELDMANN K.A., PIERCE J., BROWSE J.; | | | | |
| RT | "Cloning of higher plant omega-3 fatty acid desaturases."; | | | | |
| RL | PLANT PHYSIOL. 103:467-476(1993). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS; | | | | |
| RX | MEDLINE; 94043239. | | | | |
| RA | IBA K., GIBSON S., NISHICHI T., FUSE T., NISHIMURA M., ARONDEL V., | | | | |
| RA | HIGLY S., SOMERVILLE C.R.; | | | | |
| RT | "A gene encoding a chloroplast omega-3 fatty acid desaturase | | | | |
| RT | complements alterations in fatty acid desaturation and chloroplast | | | | |
| RT | copy number of the faty mutant of Arabidopsis thaliana."; | | | | |
| RL | J. BIOL. CHEM. 268:24099-24105(1993). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL; | | | | |
| RA | WATANAKI M., YAMAMOTO K.; | | | | |
| RT | SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS. | | | | |
| CC | -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES | | | | |
| CC | THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY | | | | |
| CC | ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT | | | | |
| CC | TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS | | | | |
| CC | ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. | | | | |
| CC | -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. | | | | |
| CC | -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). | | | | |
| CC | -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS. | | | | |
| CC | -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE | | | | |

| CC | AND/ OR BE INVOLVED IN METAL ION BINDING. |
|--------|--|
| CC | -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES. |
| CC | ----- |
| CC | CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration |
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| CC | CC or send an email to license@1sb-sib.ch). |
| CC | ----- |
| DR | EMBL: L22961; GA08481; - |
| DR | EMBL: D14007; G541653; - |
| DR | EMBL: D26019; GA68454; - |
| DR | PFAM: PF00487; FA_desaturase; 1. |
| KW | OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE; |
| KW | TRANSIT PEPTIDE. |
| FT | TRANSIT 1 ? |
| FT | CHAIN ? 446 |
| FT | OMEGA-3 FATTY ACID DESATURASE, |
| FT | CHLOROPLAST. |
| FT | HISTIDINE BOX 1. |
| FT | HISTIDINE BOX 2. |
| FT | HISTIDINE BOX 3. |
| FT | DOMAIN 199 203 |
| FT | DOMAIN 366 370 |
| FT | HISTIDINE BOX 3. |
| FT | SEQUENCE 446 AA; 51174 MW; 88DE08779 CRC32; |
| SO | SEQUENCE 446 AA; 51174 MW; 88DE08779 CRC32; |
| | Query Match 100.0%; Score 446; DB 1; Length 446; |
| | Best Local Similarity 100.0%; Pred. No. 0.00e+00; |
| | Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| D | 1 MANVLVSCGIRPLRITRITTPRNSNLSNNKFRPSLSSSYTSSPFLGNSDGFTR 60 |
| Q | 1 MANVLVSCGIRPLRITRITTPRNSNLSNNKFRPSLSSSYTSSPFLGNSDGFTR 60 |
| D | 61 MVALNSTPLTPIREESPLEEDNKRQFDPGAPFPFNADIRAAIPKHCWYNPKKSLSY 120 |
| Q | 61 MVALNSTPLTPIREESPLEEDNKRQFDPGAPFPFNADIRAAIPKHCWYNPKKSLSY 120 |
| D | 121 VVRDVAIVFALAGAAYLVNMTWPLVYLQGTMFALFVLGHDCGHSFNSDPLNSVY 180 |
| Q | 121 VVRDVAIVFALAGAAYLVNMTWPLVYLQGTMFALFVLGHDCGHSFNSDPLNSVY 180 |
| D | 181 GHLLHSSTLVYHGGRISIRHTTHQNHGVENDESNNHPSSEKLYNLDKPTREFRTPLV 240 |
| Q | 181 GHLLHSSTLVYHGGRISIRHTTHQNHGVENDESNNHPSSEKLYNLDKPTREFRTPLV 240 |
| D | 241 MLAVPYLMAASPGKSGSHYRPSDLFPRKRDVLTSTACTATAALLVCNFTIGPIQ 300 |
| Q | 241 MLAVPYLMAASPGKSGSHYRPSDLFPRKRDVLTSTACTATAALLVCNFTIGPIQ 300 |
| D | 301 MKLIGIDYWINVMWLDVFYTLHHHGHEDKLPMYRGKEMSYLRGGLTTLDRDYGILNNIH 360 |
| Q | 301 MKLIGIDYWINVMWLDVFYTLHHHGHEDKLPMYRGKEMSYLRGGLTTLDRDYGILNNIH 360 |
| D | 361 HDIGHNHVNHLFPOIPHNHLEATAAARVLAGKYRREDKSGPLRLHLEITAKIKEDH 420 |
| Q | 361 HDIGHNHVNHLFPOIPHNHLEATAAARVLAGKYRREDKSGPLRLHLEITAKIKEDH 420 |
| D | 421 YVSDGEVYVYKADPNLXGEVYKAD 446 |
| Q | 421 YVSDGEVYVYKADPNLXGEVYKAD 446 |
| RESULT | 2 |
| ID | ED3C_BRANA STANDARD; PRT: 404 AA. |
| AC | P46818; |
| DT | 01-FEB-1996 (REL. 33, CREATED) |
| DT | 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) |
| DT | 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) |
| DE | OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-) |
| DE | (FRAGMENT). |
| GN | FAD7. |
| GN | BRASSICA NAPUS (RAPE). |
| OC | EUBAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; |

| Accession | Species | Gene | Protein | Length | Score | DB 1 | DB 2 | DB 3 | DB 4 | DB 5 | DB 6 | DB 7 | DB 8 | DB 9 | DB 10 | DB 11 | DB 12 | DB 13 | DB 14 | DB 15 | DB 16 | DB 17 | DB 18 | DB 19 | DB 20 | DB 21 | DB 22 | DB 23 | DB 24 | DB 25 | DB 26 | DB 27 | DB 28 | DB 29 | DB 30 | DB 31 | DB 32 | DB 33 | DB 34 | DB 35 | DB 36 | DB 37 | DB 38 | DB 39 | DB 40 | DB 41 | DB 42 | DB 43 | DB 44 | DB 45 | DB 46 | DB 47 | DB 48 | DB 49 | DB 50 | DB 51 | DB 52 | DB 53 | DB 54 | DB 55 | DB 56 | DB 57 | DB 58 | DB 59 | DB 60 | DB 61 | DB 62 | DB 63 | DB 64 | DB 65 | DB 66 | DB 67 | DB 68 | DB 69 | DB 70 | DB 71 | DB 72 | DB 73 | DB 74 | DB 75 | DB 76 | DB 77 | DB 78 | DB 79 | DB 80 | DB 81 | DB 82 | DB 83 | DB 84 | DB 85 | DB 86 | DB 87 | DB 88 | DB 89 | DB 90 | DB 91 | DB 92 | DB 93 | DB 94 | DB 95 | DB 96 | DB 97 | DB 98 | DB 99 | DB 100 | DB 101 | DB 102 | DB 103 | DB 104 | DB 105 | DB 106 | DB 107 | DB 108 | DB 109 | DB 110 | DB 111 | DB 112 | DB 113 | DB 114 | DB 115 | DB 116 | DB 117 | DB 118 | DB 119 | DB 120 | DB 121 | DB 122 | DB 123 | DB 124 | DB 125 | DB 126 | DB 127 | DB 128 | DB 129 | DB 130 | DB 131 | DB 132 | DB 133 | DB 134 | DB 135 | DB 136 | DB 137 | DB 138 | DB 139 | DB 140 | DB 141 | DB 142 | DB 143 | DB 144 | DB 145 | DB 146 | DB 147 | DB 148 | DB 149 | DB 150 | DB 151 | DB 152 | DB 153 | DB 154 | DB 155 | DB 156 | DB 157 | DB 158 | DB 159 | DB 160 | DB 161 | DB 162 | DB 163 | DB 164 | DB 165 | DB 166 | DB 167 | DB 168 | DB 169 | DB 170 | DB 171 | DB 172 | DB 173 | DB 174 | DB 175 | DB 176 | DB 177 | DB 178 | DB 179 | DB 180 | DB 181 | DB 182 | DB 183 | DB 184 | DB 185 | DB 186 | DB 187 | DB 188 | DB 189 | DB 190 | DB 191 | DB 192 | DB 193 | DB 194 | DB 195 | DB 196 | DB 197 | DB 198 | DB 199 | DB 200 | DB 201 | DB 202 | DB 203 | DB 204 | DB 205 | DB 206 | DB 207 | DB 208 | DB 209 | DB 210 | DB 211 | DB 212 | DB 213 | DB 214 | DB 215 | DB 216 | DB 217 | DB 218 | DB 219 | DB 220 | DB 221 | DB 222 | DB 223 | DB 224 | DB 225 | DB 226 | DB 227 | DB 228 | DB 229 | DB 230 | DB 231 | DB 232 | DB 233 | DB 234 | DB 235 | DB 236 | DB 237 | DB 238 | DB 239 | DB 240 | DB 241 | DB 242 | DB 243 | DB 244 | DB 245 | DB 246 | DB 247 | DB 248 | DB 249 | DB 250 | DB 251 | DB 252 | DB 253 | DB 254 | DB 255 | DB 256 | DB 257 | DB 258 | DB 259 | DB 260 | DB 261 | DB 262 | DB 263 | DB 264 | DB 265 | DB 266 | DB 267 | DB 268 | DB 269 | DB 270 | DB 271 | DB 272 | DB 273 | DB 274 | DB 275 | DB 276 | DB 277 | DB 278 | DB 279 | DB 280 | DB 281 | DB 282 | DB 283 | DB 284 | DB 285 | DB 286 | DB 287 | DB 288 | DB 289 | DB 290 | DB 291 | DB 292 | DB 293 | DB 294 | DB 295 | DB 296 | DB 297 | DB 298 | DB 299 | DB 300 | DB 301 | DB 302 | DB 303 | DB 304 | DB 305 | DB 306 | DB 307 | DB 308 | DB 309 | DB 310 | DB 311 | DB 312 | DB 313 | DB 314 | DB 315 | DB 316 | DB 317 | DB 318 | DB 319 | DB 320 | DB 321 | DB 322 | DB 323 | DB 324 | DB 325 | DB 326 | DB 327 | DB 328 | DB 329 | DB 330 | DB 331 | DB 332 | DB 333 | DB 334 | DB 335 | DB 336 | DB 337 | DB 338 | DB 339 | DB 340 | DB 341 | DB 342 | DB 343 | DB 344 | DB 345 | DB 346 | DB 347 | DB 348 | DB 349 | DB 350 | DB 351 | DB 352 | DB 353 | DB 354 | DB 355 | DB 356 | DB 357 | DB 358 | DB 359 | DB 360 | DB 361 | DB 362 | DB 363 | DB 364 | DB 365 | DB 366 | DB 367 | DB 368 | DB 369 | DB 370 | DB 371 | DB 372 | DB 373 | DB 374 | DB 375 | DB 376 | DB 377 | DB 378 | DB 379 | DB 380 | DB 381 | DB 382 | DB 383 | DB 384 | DB 385 | DB 386 | DB 387 | DB 388 | DB 389 | DB 390 | DB 391 | DB 392 | DB 393 | DB 394 | DB 395 | DB 396 | DB 397 | DB 398 | DB 399 | DB 400 | DB 401 | DB 402 | DB 403 | DB 404 | DB 405 | DB 406 | DB 407 | DB 408 | DB 409 | DB 410 | DB 411 | DB 412 | DB 413 | DB 414 | DB 415 | DB |
|-----------|---------|------|---------|--------|-------|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----|
|-----------|---------|------|---------|--------|-------|------|------|------|------|------|------|------|------|------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----|

| | | |
|----|--|-----------|
| RX | MEDLINE | 94302177. |
| RA | VAN DE LOO F.J., SOMERVILLE C.R.; | |
| RT | "Plasmod omega-3 fatty acid desaturase cDNA from <i>Ricinus communis</i> ."; | |
| RL | PLANT PHYSIOL. 105:443-444(1994). | |
| CC | -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGH TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. | |
| CC | -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. | |
| CC | -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). | |
| CC | -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/ OR BE INVOLVED IN METAL ION BINDING. | |
| CC | -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASIS. | |
| CC | ----- | |
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| CC | ----- | |
| DR | EMBL; L25897; G414732; . | |
| DR | PFAM; PF00487; FA_desaturase; 1. | |
| DR | OXIDOREDUCTASE: FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE; | |
| KW | TRANSIT PEPTIDE. | |
| FT | TRANST | |
| FT | 1 ? | |
| FT | CHAIN 1 460 CHLOROPLAST (POTENTIAL), | |
| FT | CHLOROPLAST, | |
| FT | DOMAIN 177 181 HISTIDINE BOX 1. | |
| FT | DOMAIN 213 217 HISTIDINE BOX 2. | |
| FT | DOMAIN 380 384 HISTIDINE BOX 3. | |
| QD | SEQUENCE 460 AA; 52561 MW; D83DA689 CRC32; | |

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Query Match          9.9%:  Score 44;  DB 1;  Length 460;
Best Local Similarity 100.0%:  Pred. No. 5,10e-116;
Matches      44;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Db      188  PKLNSVGHLLSSILVPGHGRMISHRTTHONHGHVDESMHP 231
      |||||||
QY      174  PKLNSVGHLLSSILVPGHGRMISHRTTHONHGHVDESMHP 217

RESULT      4
ID      FD3D_ARATH      STANDARD:      PRT;      435 AA.
AC      P46822;
DT      01-FEB-1996 (REL. 33, CREATED)
DT      01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT      01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE      TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
      PRECURSOR (Ec.1.14.99.-).
GN      Fd8.
OS      ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC      EUPHAROTIA: VIRIDIPLANTAE: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES.
OC      EUPHYLLIPHYTES: SPEEMAMOPHYTA: MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC      CAPRARALES; BRASSICACEAE; ARABIDOPSIS.
      [1]
RN      SEQUENCE FROM N.A.
RP      STRAIN-CV, COLUMBIA; TISSUE=AFRICAL PARTS;
RC      MEDLINE; 95148742.
RX      GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
      "Cloning of a temperature-regulated gene encoding a chloroplast
      omega-3 desaturase from Arabidopsis thaliana.";
      PLANT PHYSIOL. 106:1615-1621(1994).
      [2]
RN      SEQUENCE FROM N.A.
RP      STRAIN-CV, COLUMBIA; TISSUE=HYPOCOTYL;
RC      WATAHAKI M.C., YAMAMOTO K.T.;
      SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC      -I- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
      THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
      ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT

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| | | |
|----|---|--|
| CC | | TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS. |
| CC | | ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. |
| CC | -1- | PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. |
| CC | -1- | SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). |
| CC | -1- | INDUCTION: BY LOW TEMPERATURES. |
| CC | -1- | DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE AND/OR BE INVOLVED IN METAL ION BINDING. |
| CC | -1- | SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES. |
| CC | | ----- |
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| CC | | ----- |
| DR | EMBL; L27158; | G516045; - |
| DR | EMBL; U08216; | G497219; - |
| DR | EMBL; D17578; | G471093; - |
| KW | OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE; | |
| FT | TRANSIT PEPTIDE. | |
| FT | TRANSIT | 1 |
| FT | CHAIN | ? 435 |
| FT | | CHLOROPLAST (POTENTIAL); |
| FT | | TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID |
| FT | | DESATURASE; CHLOROPLAST. |
| FT | DOMAIN | 156 160 HISTIDINE BOX 1. |
| FT | DOMAIN | 192 196 HISTIDINE BOX 2. |
| FT | DOMAIN | 359 363 HISTIDINE BOX 3. |
| NO | SEQUENCE | 435 AA; 50136 MW; 70613PF0 CRC32; |

Query Match 9.6%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,56e-112;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNIHHDIGTGVHIIHLPQIPHYHLVTEATEAKPKYKREP 391
OY 356 INNIHHDIGTGVHIIHLPQIPHYHLVTEATEAKPKYKREP 398
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|||||

RESULT 5
ID PD3C, SESIN STANDARD; PRT; 447 AA.
AC P46820;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOPOPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY).
OC EUPAROTIA, VIRIDIPLANTAE; STREPTOPHYTA; EMRYOPHYTA;
OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALIACEAE; SESAMUM.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV. 4294; TISSUE-COTYLEDON;
RL SHOJI K.;
RA SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOPOPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERRODOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOPLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOPOPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL: U25817; G870784; -
 KW PFMAM; PF00487; FA_desaturase; 1.
 CC OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KW TRANSIT PEPTIDE.
 FT TRANSIT 1.
 FT CHAIN ? 447 CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE,
 FT CHAIN ? 447 CHLOROPLAST.
 FT DOMAIN 167 171 HISTIDINE BOX 1.
 FT DOMAIN 203 207 HISTIDINE BOX 2.
 FT DOMAIN 370 374 HISTIDINE BOX 3.
 SQ SEQUENCE 447 AA; 5116 MM; 67B2C46B CRC32;
 Query Match 8.1%; Score 36; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.56e-88;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 323 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 358
 319 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 354
 QY 319 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 354
 RESULT 6
 ID FD3C_S0YBN STANDARD; PRT; 453 AA.
 AC P46621;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 GN FAD7.
 OS GLYCINE MAX (SOYBEAN).
 CC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL: L22965; G408792; -
 DR PIR: J02339; J02339
 DR PFMAM; PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KW TRANSIT PEPTIDE.
 FT TRANSIT 1.
 FT CHAIN ? 453 CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 453 OMEGA-3 FATTY ACID DESATURASE,
 FT CHAIN ? 453 CHLOROPLAST.
 FT DOMAIN 171 175 HISTIDINE BOX 1.

FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT DOMAIN 374 378 HISTIDINE BOX 3.
 SQ SEQUENCE 453 AA; 51362 MM; E4314F1B CRC32;
 Query Match 8.1%; Score 36; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 2.56e-88;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 327 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 362
 319 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 354
 QY 319 VTYLHHGHEDKLPYRGKEMSYLRGGLTTLD RDYG 354
 RESULT 7
 ID FD31_BRANA STANDARD; PRT; 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (VERSION 1).
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 CC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPPARALES; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC or send an email to license@lsb-sib.ch).
 CC -----
 DR EMBL: L22962; G408492; -
 DR PFMAM; PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSFERASE.
 FT TRANSFER 54 73 POTENTIAL.
 FT TRANSFER 203 226 POTENTIAL.
 FT TRANSFER 233 251 POTENTIAL.
 FT TRANSFER 92 96 HISTIDINE BOX 1.
 FT DOMAIN 128 132 HISTIDINE BOX 2.
 FT DOMAIN 295 299 HISTIDINE BOX 3.
 SQ SEQUENCE 377 AA; 43258 MM; 247337E0 CRC32;
 Query Match 6.3%; Score 28; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.56e-61;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 117 ILVYHGMRIKSHRTHQHGHVDESM 144


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OY 188 ILVYHGMRIKSHRTNHNHGVNDESM 215
|||||
RESULT 8
ID FD32.BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE);
OC EUKARYOTA: VIRIDIPANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC CAPRALES: BRASSICACEAE; BRASSICA.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMEVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
CC EMBL: L01418; G167148; -
CC FRAM: PF00487; FA.desaturase: 1.
CC OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC KW TRANSMEM.
CC FT TRANSMEM 53 73 POTENTIAL.
CC FT TRANSMEM 210 230 POTENTIAL.
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 98 102 HISTIDINE BOX 1.
CC FT DOMAIN 134 138 HISTIDINE BOX 2.
CC FT DOMAIN 301 305 HISTIDINE BOX 3.
CC SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32.

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Query Match 6.3%; Score 28; DB 1; Length 383;
 Best Local Similarity 100.0%; Pred. No. 2,356-61;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GN FAD3 OR F23F1.10.
OS AAABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC CAPRALES: BRASSICACEAE; ARABIDOPSIS.
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA; TISSUE-SEEDLING;
RX MEDLINE: 94302147.
RA YADAV N.S., WIRZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN (2)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAIKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN (3)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA;
RX MEDLINE: 94345020.
RA NISHIUCHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 105:767-768(1994).
RN (4)
RP SEQUENCE FROM N.A.
RX STRAIN-CV. COLUMBIA;
RA ROUNDSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA SYKES S.M., KAIL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMEVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
CC EMBL: L22931; G408483; -
CC DR EMBL: D17579; G471091; -
CC DR EMBL: D26508; G1197795; -
CC DR EMBL: AC004680; G3420053; -
CC FRAM: PF00487; FA.desaturase: 1.
CC OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC KW TRANSMEM.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 220 240 POTENTIAL.
CC FT TRANSMEM 242 262 POTENTIAL.
CC FT DOMAIN 101 105 HISTIDINE BOX 1.
CC FT DOMAIN 137 141 HISTIDINE BOX 2.
CC FT DOMAIN 304 308 HISTIDINE BOX 3.
CC SQ SEQUENCE 386 AA; 44076 MW; C22B48BC CRC32.

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Query Match 6.3%; Score 28; DB 1; Length 386;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV, SRI; TISSUE-LEAF;
RX MEDLINE: 95011632.
RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.;
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
RL GENE 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLED BOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: D26509; G599592; -
DR PRAM: P000487; FA.Desaturase: 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;
Query Match 5.4%; Score 24; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3,27E-48;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 291 NNHHDIGTHVHHLFQIPHYHL 314
QY 357 NNHHDIGTHVHHLFQIPHYHL 380
RESULT 13
ID RL1.TREPA STANDARD; PRT; 226 AA.
AC 083266;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L1.
GN RPLA OR TP0238.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAR H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL SCIENCE 281:375-388(1998).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS

CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: AE001205; G3322508; -
DR TIGR: TP0238; -
DR PROSITE: PS01199; RIBOSOMAL.L1; 1.
KW RIBOSOMAL PROTEIN; RNA-BINDING.
SQ SEQUENCE 226 AA; 24977 MW; 423DB8A1 CRC32;
Query Match 1.8%; Score 8; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 2,29E-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 83 ALAAGAY 90
QY 130 ALAAGAY 137
RESULT 14
ID KNR.DROME STANDARD; PRT; 429 AA.
AC P10734;
DT 01-JUL-1989 (REL. 11, CREATED)
DT 01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE ZYGOTIC GAP PROTEIN KNRPS.
GN KNT.
OS DROSOPHILA MELANOGASTER (FRUIT FLY).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
OC PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON-R; TISSUE-SALIVARY GLAND;
RX MEDLINE: 89057148.
RA NAUMER U., PANKRATZ M.J., KILNLIN A., SEYFFERT E., KLEMM U.,
RA JACKLE H.;
RT "Abdominal segmentation of the Drosophila embryo requires a hormone
RT receptor-like protein encoded by the gap gene knirps.";
RL NATURE 336:489-492(1988).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE: 96312963.
RA ARNOSTI D.N., GRAY S., BAROLO S., ZHOU J., LEVINE M.;
RT "The gap protein knirps mediates both quenching and direct repression
RT in the Drosophila embryo.";
RL EMBO J. 15:3659-3666(1996).
CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS TO MULTIPLE SITES IN
CC THE EVE STRIPE 3 ENHANCER ELEMENT. PLAYS AN ESSENTIAL ROLE IN THE
CC SEGMENTATION PROCESS BOTH BY REFINING THE EXPRESSION PATTERNS OF
CC GAP GENES AND BY ESTABLISHING PAIR-RULES STRIPES OF GENE
CC EXPRESSION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC -----
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CC -----
DR EMBL: X13331; G8154; -
DR PIR: S01919; S01919.

DR FLYBASE: FBgn0001320; kn1.
 DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
 DR PFAW: PF00105; ZF-C4; 1.
 DR HSSP: P03372; IHCO.
 DR TRANSFAC: T00445; "-
 KW RECEPTOR: TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN;
 KZ ZINC-FINGER: DEVELOPMENTAL PROTEIN; REPRESSOR.
 FT DNA_BIND 5 71 C4-TYPE ZINC FINGERS (TWO).
 FT ZN_FING 5 25 C4-TYPE.
 FT ZN_FING 42 66 C4-TYPE.
 FT DOMAIN 97 101 POLY-ALA.
 FT DOMAIN 137 142 POLY-HIS.
 FT DOMAIN 143 149 POLY-GLN.
 FT DOMAIN 200 213 POLY-ALA.
 FT DOMAIN 375 382 POLY-SER.
 SO SEQUENCE 429 AA; 45611 MW; 519CEDE CRC32;

Query Match 1.8%; Score 8; DB 1; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2,29e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 288 TSSPLSF 295
 QY 43 TSSPLSF 50

RESULT 15
 ID RL27_STRGR STANDARD; PRT; 85 AA.
 AC P95757;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L27.
 GN RPLA.
 OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189;
 RX MEDLINE; 97136618.
 RA OKAMOTO S., ITOH M., OCHI K.;
 RT "Molecular cloning and characterization of the obg gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation.";
 RL J. BACTERIOL. 179:170-179(1997).
 CC -I- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: D87916; GI/83293; -
 DR PROSITE: PS00831; RIBOSOMAL_L27; 1.
 DR PFAW: PF01016; Ribosomal_L27; 1.
 KW RIBOSOMAL PROTEIN.
 SO SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.6%; Score 7; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2,28e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAAGA 66
 QY 129 FALAAGA 135

Search completed: Sat Aug 21 12:12:52 1999
 Job time : 49 secs.

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:13:11 1999; MasPar time 25.58 Seconds

Tabular output not generated. 951.471 Million cell updates/sec

Title: >US-09-219-935-5
 Description: (1-446) from US09219935.pep
 Perfect Score: 446

Sequence: 1 MANVLVSEGGIRPLRIYTT.....EYVYKADPNLYGEVYKVRAD 446

Scoring table: TABLE uniprottable

Gap 60

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

aplysmbl9;
 1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
 5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
 9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
 13:sp-vertebrate 14:sp-virus

Statistics: Mean 3.676; Variance 0.439; scale 8.381

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-----------|------------------------|-----------|
| 1 | 47 | 10.5 | 436 | 10 Q40118 | DELTA-15 LINCOLN DESAT | 2.75e-121 |
| 2 | 43 | 9.6 | 398 | 10 Q24626 | FATTY ACID DESATURASE | 7.08e-108 |
| 3 | 40 | 9.0 | 431 | 10 C82068 | W-3 DESATURASE | 6.87e-98 |
| 4 | 40 | 9.0 | 441 | 10 P93350 | OMEGA-3 FATTY ACID DES | 5.63e-88 |
| 5 | 37 | 8.3 | 438 | 10 C04807 | FATTY ACID DESATURASE | 1.09e-84 |
| 6 | 36 | 8.1 | 443 | 10 Q23824 | FATTY ACID DESATURASE | 5.63e-88 |
| 7 | 34 | 7.6 | 438 | 10 P93452 | OMEGA-3 FATTY ACID DES | 3.80e-78 |
| 8 | 29 | 6.5 | 381 | 10 P94013 | W-3 FATTY ACID DESATUR | 5.36e-62 |
| 9 | 29 | 6.5 | 383 | 10 C65792 | OMEGA-3 FATTY ACID DES | 5.36e-62 |
| 10 | 28 | 6.3 | 407 | 10 C64907 | OMEGA-3 DESATURASE (FR | 8.26e-59 |
| 11 | 24 | 5.4 | 380 | 10 Q23802 | PLASTID OMEGA-3 FATTY | 3.10e-46 |
| 12 | 16 | 3.6 | 359 | 2 C05240 | DELTA 15 DESATURASE | 2.51e-22 |
| 13 | 11 | 2.5 | 350 | 2 C07872 | OMEGA-3 DESATURASE | 6.41e-09 |
| 14 | 9 | 2.0 | 494 | 5 C017121 | M151.1 PROTEIN | 3.43e-04 |
| 15 | 8 | 1.8 | 193 | 3 C074645 | FATTY ACID DESATURASE | 4.83e-02 |
| 16 | 8 | 1.8 | 445 | 5 C023091 | SIMILAR TO NADPH DEHYD | 4.83e-02 |
| 17 | 8 | 1.8 | 598 | 2 C04316 | MALTOLOGOSYD TREHALOS | 4.83e-02 |
| 18 | 8 | 1.8 | 1313 | 3 P87141 | PUTATIVE GUANINE-NUCLE | 4.83e-02 |
| 19 | 8 | 1.8 | 4848 | 2 C007944 | PRISTINAMYCIN I SYNTHA | 4.83e-02 |
| 20 | 7 | 1.6 | 193 | 3 C012064 | D1554 | 4.40e+00 |

| | | | | | | | |
|----|---|-----|------|----|--------|------------------------|----------|
| 21 | 7 | 1.6 | 212 | 1 | 059378 | 212AA LONG HYPOTHETICA | 4.40e+00 |
| 22 | 7 | 1.6 | 241 | 8 | 063069 | RIBULOSE BISPHOSPHATE | 4.40e+00 |
| 23 | 7 | 1.6 | 257 | 2 | 066760 | HYPOTHETICAL 29.7 KD P | 4.40e+00 |
| 24 | 7 | 1.6 | 305 | 2 | 050934 | CONSERVED HYPOTHETICAL | 4.40e+00 |
| 25 | 7 | 1.6 | 351 | 3 | 074180 | ALTERNATIVE OXIDASE | 4.40e+00 |
| 26 | 7 | 1.6 | 402 | 8 | 047071 | RIBULOSE BISPHOSPHATE | 4.40e+00 |
| 27 | 7 | 1.6 | 402 | 8 | 047074 | RIBULOSE BISPHOSPHATE | 4.40e+00 |
| 28 | 7 | 1.6 | 402 | 8 | 047079 | RIBULOSE BISPHOSPHATE | 4.40e+00 |
| 29 | 7 | 1.6 | 426 | 5 | 024442 | (CDNA3) PROTEIN 4.1 HO | 4.40e+00 |
| 30 | 7 | 1.6 | 428 | 10 | 080351 | S GLYCOPROTEIN (FRAGME | 4.40e+00 |
| 31 | 7 | 1.6 | 429 | 10 | 023851 | S GLYCOPROTEIN (FRAGME | 4.40e+00 |
| 32 | 7 | 1.6 | 649 | 3 | 007655 | COSMOSOME IV READING | 4.40e+00 |
| 33 | 7 | 1.6 | 705 | 3 | 019547 | COSMID F18C5 | 4.40e+00 |
| 34 | 7 | 1.6 | 716 | 2 | 049526 | LYMP6P | 4.40e+00 |
| 35 | 7 | 1.6 | 754 | 3 | 002845 | YRBP | 4.40e+00 |
| 36 | 7 | 1.6 | 824 | 4 | 093138 | VIRAL GLYCOPROTEIN H. | 4.40e+00 |
| 37 | 7 | 1.6 | 824 | 4 | 075286 | K1A0345-LIKE 11 | 4.40e+00 |
| 38 | 7 | 1.6 | 864 | 10 | 049329 | SIMILAR TO DISEASE RES | 4.40e+00 |
| 39 | 7 | 1.6 | 934 | 4 | 015046 | K1A0338 (FRAGMENT) | 4.40e+00 |
| 40 | 7 | 1.6 | 962 | 2 | 049546 | IMP1 AND IMP2 GENES | 4.40e+00 |
| 41 | 7 | 1.6 | 1246 | 14 | 089604 | U130 (EC 2.7.7.7). | 4.40e+00 |
| 42 | 7 | 1.6 | 1365 | 2 | 049525 | IMP1 | 4.40e+00 |
| 43 | 7 | 1.6 | 1698 | 5 | 024440 | (CDNA1) PROTEIN 4.1 HO | 4.40e+00 |
| 44 | 7 | 1.6 | 1840 | 11 | 061818 | HYPOTHETICAL 196.0 KD | 4.40e+00 |
| 45 | 7 | 1.6 | 2569 | 2 | 087313 | FXBB | 4.40e+00 |

ALIGNMENTS

RESULT 1
 ID Q40118; PRELIMINARY; PRT; 436 AA.

AC 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE DELTA-15 LINCOLN DESATURASE.
 OS LIMNANTHES DOUGLASSII.
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAMPARALES; LIMNANTHACEAE; LIMNANTHES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 95334518.
 RX BHELIA R.S., MACKENZIE S.L.;
 RT "Nucleotide sequence of a cDNA from Limnanthus douglasii L. encoding
 a delta-15 linoleic acid desaturase."
 RL PLANT PHYSIOL. 108:861-861(1995).
 DR EMBL; U17063; G699390; .
 DR PFWM; PF00487; FA_desaturase; 1.
 DR MENDEL; 8699; LIMDO; 1208; 1.
 SO SEQUENCE 436 AA; 50093 MW; 327D77FE CMC32;

Query Match 10.5%; Score 47; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 2.75e-121;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 330 EWSYLRGGLTLDROYGLINNHHIDSTHYIHLFPDIPRYHLVEAT 376
 338 EWSYLRGGLTLDROYGLINNHHIDSTHYIHLFPDIPRYHLVEAT 384

RESULT 2
 ID Q24626; PRELIMINARY; PRT; 398 AA.
 AC 024626;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE FATTY ACID DESATURASE (FRAGMENT).
 GN FAD8
 OS ZEA MAYS (MAIZE).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
 OC POACEAE; ZEA.

Query Match 8.1%; Score 36; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 1,09e-84;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTUHHHGHEDKLPWYRGKWSYLGGLTLDROG 352
OY 319 VTUHHHGHEDKLPWYRGKWSYLGGLTLDROG 354

RESULT 7
ID P93452 PRELIMINARY; PRT; 438 AA.
AC P93452;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE
OS PETROSELINUM CRISPRUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUDAROTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; ARALIALES; APIACEAE; PETROSELINUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97203190.
RA KIRSCH C., TAKAMURA WIK M., REINOLD S., HAHNBROCK K., SOMSSICH I.E.;
RT "Rapid, transient, and highly localized induction of plastidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
DR EMBL; U75745; G1786066; -;
DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9788; PTCR:1208;1.
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;

Query Match 7.6%; Score 34; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 3,80e-78;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 180 LHSILVYHGMWIRSHRTNHNHGHVDESWHP 213
OY 184 LHSILVYHGMWIRSHRTNHNHGHVDESWHP 217

RESULT 8
ID P94013 PRELIMINARY; PRT; 381 AA.
AC P94013;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE W-3 FATTY ACID DESATURASE.
OS ORYZA SATIVA (RICE).
OC EUDAROTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ORYZA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IR36, AND NIPPONBARE;
RA AKAGI H.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; D78506; G1777376; -;
DR EMBL; D78505; G1785856; -;
DR MENDEL; 9612; ORYSA:1208;1.
SQ SEQUENCE 381 AA; 43640 MW; 2BD4ED6E CRC32;

Query Match 6.5%; Score 29; DB 10; Length 381;
Best Local Similarity 100.0%; Pred. No. 5,36e-62;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 288 INNHHDIGTHVHHLFPOIPHYHLEAF 316
OY 356 INNHHDIGTHVHHLFPOIPHYHLEAF 384

RESULT 9

ID 065792 PRELIMINARY; PRT; 383 AA.
AC 065792;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN TAFAD3.
OS TRITICUM AESTIVUM (WHEAT).
OC EUDAROTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU, TISSUE-LEAF, AND ROOT;
RA HORIGUCHI G., KAWAKAMI N., KUSUMI K., KODAMA H., IBA K.;
RL PLANT CELL PHYSIOL. 39:540-544(1998).
DR EMBL; D84678; D1029298; -;
SQ SEQUENCE 383 AA; 43687 MW; 50D38F40 CRC32;

Query Match 6.5%; Score 29; DB 10; Length 383;
Best Local Similarity 100.0%; Pred. No. 5,36e-62;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 INNHHDIGTHVHHLFPOIPHYHLEAF 318
OY 356 INNHHDIGTHVHHLFPOIPHYHLEAF 384

RESULT 10
ID 064907 PRELIMINARY; PRT; 407 AA.
AC 064907;
DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE (FRAGMENT).
GN PXH-15.
OS PELARGONIUM X HORTORUM.
OC EUDAROTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC GERANIACEAE; PELARGONIUM.
RN [1]
RP SEQUENCE FROM N.A.
RA SCHULTZ D.J., MOMMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AF020204; G3133289; -;
FT NON_TER
SQ SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;

Query Match 6.3%; Score 28; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 8,26e-59;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 318 NNHHDIGTHVHHLFPOIPHYHLEAF 345
OY 357 NNHHDIGTHVHHLFPOIPHYHLEAF 384

RESULT 11
ID 023802 PRELIMINARY; PRT; 380 AA.
AC 023802;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
GN TAFAD7.
OS TRITICUM AESTIVUM (WHEAT).
OC EUDAROTA, VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU, TISSUE-LEAF;
RA HORIGUCHI G., TAKAKAWA H., KODAMA H., NISHIMURA M.,

RA IBA K.;
RL PHYSIOL. PLANTARUM 96:275-283(1996).
DR EMBL: D43688; D1008371; -.
DR PFAM: PF00487; FA_desaturase; 1.
FT NON-TER 1
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;
Query Match 5.4%; Score 24; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 3.10e-46;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 130 GWRISHRTHONGHVENDESNHP 153
OY 194 GWRISHRTHONGHVENDESNHP 217
RESULT 12
ID 055240; PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
GN DESB.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
RA MURATA N.;
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
RT altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANKO T., SATO S., KOTANI H., TANAKA A., ASAMITU E., NAKAMURA Y.,
RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
RA HOSUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARDO K., OKUMURA S.,
RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
RA TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-116(1996).
DR EMBL: D13780; G600598; -.
DR EMBL: D90913; G1653388; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;
Query Match 3.6%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 2.51e-22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 114 ILVPHGWRISHRTH 129
OY 188 ILVPHGWRISHRTH 203
RESULT 13
ID 007872; PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCCLUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCCLUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
RT acid desaturase genes in the cyanobacterium Synechococcus sp. strain
RT PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL: U36389; G2197199; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;
Query Match 2.5%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 6.41e-09;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 74 AOGTFMFLFY 84
OY 150 AOGTFMFLFY 160
RESULT 14
ID 017121; PRELIMINARY; PRT; 494 AA.
AC 017121;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE M151.1 PROTEIN.
GN M151.1.
OS CAENORHABDITIS ELEGANS.
OC EUDAROTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA GRAYTON M., DEAR S., DU Z., DURBIN R., FAYELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLER L., JIR M., JOHNSTON L.,
RA JONES M., KESHAM J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LITCHING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHIDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL NATURE 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA GARTUNG S., GOELA D.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF024502; G2394495; -.
SQ SEQUENCE 494 AA; 57632 MW; 186202ED CRC32;
Query Match 2.0%; Score 9; DB 5; Length 494;
Best Local Similarity 100.0%; Pred. No. 3.43e-04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 295 SSSSYKTS 303
OY 37 SSSSYKTS 45
RESULT 15

ID 074645 PRELIMINARY; PRT: 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLEREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLEREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLEREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEAE.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-F15;
RX MEDLINE; 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
RT Analysis of the region around Trl101 and characterization of its
RT homologue from Fusarium sporotrichioides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 193
SO SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 1.8%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred.No. 4.83e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 186 HVTHLFP 193
 |||||||
OY 366 HVTHLFP 373

Search completed: Sat Aug 21 12:15:00 1999
Job time : 109 secs.

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MSPrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:06:37 1999; MasPar time 16.89 Seconds
561.475 Million cell updates/sec

Tabular output not generated.

Title: >US-09-219-935-5

Description: (1-446) from US09219935.pep

Sequence: 1 MANLVSECGIRPLRITYT.....EVVYKADPNLXGEVKNRAD 446

Scoring table: TABLE uniprottable
Gap 60

Searched: 170751 segs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a:geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.955; Variance 0.700; scale 4.224

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------|
| 1 | 446 | 100.0 | 446 | 11 | R60499 | 0.00e+00 |
| 2 | 446 | 100.0 | 446 | 7 | R37593 | 0.00e+00 |
| 3 | 103 | 23.1 | 378 | 7 | R37591 | 2.98e-162 |
| 4 | 103 | 23.1 | 404 | 7 | R37594 | 2.98e-162 |
| 5 | 43 | 9.6 | 435 | 11 | R60500 | 1.59e-56 |
| 6 | 35 | 8.1 | 447 | 24 | W13381 | 1.46e-44 |
| 7 | 36 | 8.1 | 453 | 7 | R37596 | 1.46e-44 |
| 8 | 29 | 6.3 | 156 | 7 | R37598 | 8.60e-33 |
| 9 | 28 | 6.3 | 383 | 11 | R60498 | 3.94e-31 |
| 10 | 28 | 6.3 | 386 | 7 | R37592 | 3.94e-31 |
| 11 | 27 | 6.1 | 380 | 7 | R37595 | 1.78e-29 |
| 12 | 27 | 6.1 | 126 | 7 | R37597 | 7.87e-02 |
| 13 | 8 | 1.8 | 120 | 14 | R80294 | 1.46e+00 |
| 14 | 8 | 1.8 | 597 | 14 | R80290 | 1.46e+00 |
| 15 | 8 | 1.8 | 598 | 14 | R77471 | 1.46e+00 |
| 16 | 7 | 1.6 | 18 | 8 | R38424 | 2.30e+01 |

| 17 | 1.6 | 18 | 2 | R07633 | N-terminal of Fractin | 2.30e+01 |
|---|--|------|----|--------|---|----------|
| 18 <td>1.6<td>18</td><td>17</td><td>R88585</td><td>Spider venom calcium<th>2.30e+01</th></td></td> | 1.6 <td>18</td> <td>17</td> <td>R88585</td> <td>Spider venom calcium<th>2.30e+01</th></td> | 18 | 17 | R88585 | Spider venom calcium <th>2.30e+01</th> | 2.30e+01 |
| 19 <td>1.6<td>367</td><td>34</td><td>W61492</td><td>Human fetuin glycopro<th>2.30e+01</th></td></td> | 1.6 <td>367</td> <td>34</td> <td>W61492</td> <td>Human fetuin glycopro<th>2.30e+01</th></td> | 367 | 34 | W61492 | Human fetuin glycopro <th>2.30e+01</th> | 2.30e+01 |
| 20 <td>1.6<td>663</td><td>4</td><td>R24101</td><td>Marek's disease virus<th>2.30e+01</th></td></td> | 1.6 <td>663</td> <td>4</td> <td>R24101</td> <td>Marek's disease virus<th>2.30e+01</th></td> | 663 | 4 | R24101 | Marek's disease virus <th>2.30e+01</th> | 2.30e+01 |
| 21 <td>1.6<td>789</td><td>18</td><td>R35603</td><td>STP4 (suppressor of t<th>2.30e+01</th></td></td> | 1.6 <td>789</td> <td>18</td> <td>R35603</td> <td>STP4 (suppressor of t<th>2.30e+01</th></td> | 789 | 18 | R35603 | STP4 (suppressor of t <th>2.30e+01</th> | 2.30e+01 |
| 22 <td>1.3</td> <td>21</td> <td>14</td> <td>R73894</td> <td>Listeria monocytogene<th>2.35e+02</th></td> | 1.3 | 21 | 14 | R73894 | Listeria monocytogene <th>2.35e+02</th> | 2.35e+02 |
| 23 <td>1.3</td> <td>65</td> <td>38</td> <td>W88611</td> <td>Secreted protein enco<th>2.35e+02</th></td> | 1.3 | 65 | 38 | W88611 | Secreted protein enco <th>2.35e+02</th> | 2.35e+02 |
| 24 <td>1.3</td> <td>81</td> <td>37</td> <td>W75089</td> <td>Human secreted protei<th>2.35e+02</th></td> | 1.3 | 81 | 37 | W75089 | Human secreted protei <th>2.35e+02</th> | 2.35e+02 |
| 25 <td>1.3</td> <td>128</td> <td>39</td> <td>W84336</td> <td>Protein N of PRSV is<th>2.35e+02</th></td> | 1.3 | 128 | 39 | W84336 | Protein N of PRSV is <th>2.35e+02</th> | 2.35e+02 |
| 26 <td>1.3</td> <td>157</td> <td>3</td> <td>R20094</td> <td>Pf16 surface protein<th>2.35e+02</th></td> | 1.3 | 157 | 3 | R20094 | Pf16 surface protein <th>2.35e+02</th> | 2.35e+02 |
| 27 <td>1.3</td> <td>159</td> <td>37</td> <td>W81766</td> <td>E. coli DHR-EC pep1<th>2.35e+02</th></td> | 1.3 | 159 | 37 | W81766 | E. coli DHR-EC pep1 <th>2.35e+02</th> | 2.35e+02 |
| 28 <td>1.3</td> <td>202</td> <td>39</td> <td>W67822</td> <td>Human secreted protei<th>2.35e+02</th></td> | 1.3 | 202 | 39 | W67822 | Human secreted protei <th>2.35e+02</th> | 2.35e+02 |
| 29 <td>1.3</td> <td>203</td> <td>39</td> <td>W67898</td> <td>Human secreted protei<th>2.35e+02</th></td> | 1.3 | 203 | 39 | W67898 | Human secreted protei <th>2.35e+02</th> | 2.35e+02 |
| 30 <td>1.3</td> <td>398</td> <td>36</td> <td>W13368</td> <td>Death associated prot<th>2.35e+02</th></td> | 1.3 | 398 | 36 | W13368 | Death associated prot <th>2.35e+02</th> | 2.35e+02 |
| 31 <td>1.3</td> <td>438</td> <td>39</td> <td>W95500</td> <td>B. subtilis Yade rela<th>2.35e+02</th></td> | 1.3 | 438 | 39 | W95500 | B. subtilis Yade rela <th>2.35e+02</th> | 2.35e+02 |
| 32 <td>1.3</td> <td>440</td> <td>24</td> <td>W12826</td> <td>Rat Sox-4</td> <th>2.35e+02</th> | 1.3 | 440 | 24 | W12826 | Rat Sox-4 | 2.35e+02 |
| 33 <td>1.3</td> <td>459</td> <td>39</td> <td>W73477</td> <td>Grapevine leafroll vi<th>2.35e+02</th></td> | 1.3 | 459 | 39 | W73477 | Grapevine leafroll vi <th>2.35e+02</th> | 2.35e+02 |
| 34 <td>1.3</td> <td>462</td> <td>38</td> <td>W81964</td> <td>Human RAR-alpha prote<th>2.35e+02</th></td> | 1.3 | 462 | 38 | W81964 | Human RAR-alpha prote <th>2.35e+02</th> | 2.35e+02 |
| 35 <td>1.3</td> <td>477</td> <td>36</td> <td>W80695</td> <td>S. pneumoniae hydroph<th>2.35e+02</th></td> | 1.3 | 477 | 36 | W80695 | S. pneumoniae hydroph <th>2.35e+02</th> | 2.35e+02 |
| 36 <td>1.3</td> <td>512</td> <td>39</td> <td>W87797</td> <td>Protease encoded by c<th>2.35e+02</th></td> | 1.3 | 512 | 39 | W87797 | Protease encoded by c <th>2.35e+02</th> | 2.35e+02 |
| 37 <td>1.3</td> <td>549</td> <td>38</td> <td>W70898</td> <td>Acetyl-coenzyme A tra<th>2.35e+02</th></td> | 1.3 | 549 | 38 | W70898 | Acetyl-coenzyme A tra <th>2.35e+02</th> | 2.35e+02 |
| 38 <td>1.3</td> <td>707</td> <td>38</td> <td>W83395</td> <td>Rabbit protein couple<th>2.35e+02</th></td> | 1.3 | 707 | 38 | W83395 | Rabbit protein couple <th>2.35e+02</th> | 2.35e+02 |
| 39 <td>1.3</td> <td>749</td> <td>37</td> <td>W80359</td> <td>Helicobacter pylori U<th>2.35e+02</th></td> | 1.3 | 749 | 37 | W80359 | Helicobacter pylori U <th>2.35e+02</th> | 2.35e+02 |
| 40 <td>1.3</td> <td>797</td> <td>38</td> <td>W81963</td> <td>Human myl/RAR-alpha f<th>2.35e+02</th></td> | 1.3 | 797 | 38 | W81963 | Human myl/RAR-alpha f <th>2.35e+02</th> | 2.35e+02 |
| 41 <td>1.3</td> <td>870</td> <td>38</td> <td>W73485</td> <td>Human myl/RAR-alpha f<th>2.35e+02</th></td> | 1.3 | 870 | 38 | W73485 | Human myl/RAR-alpha f <th>2.35e+02</th> | 2.35e+02 |
| 42 <td>1.3</td> <td>907</td> <td>14</td> <td>W95395</td> <td>Human myl/RAR-alpha f<th>2.35e+02</th></td> | 1.3 | 907 | 14 | W95395 | Human myl/RAR-alpha f <th>2.35e+02</th> | 2.35e+02 |
| 43 <td>1.3</td> <td>1012</td> <td>39</td> <td>R80144</td> <td>EBV gp350/220</td> <th>2.35e+02</th> | 1.3 | 1012 | 39 | R80144 | EBV gp350/220 | 2.35e+02 |
| 44 <td>1.3</td> <td>1347</td> <td>37</td> <td>W81506</td> <td>IBDV VP2-VP3-VP4 poly<th>2.35e+02</th></td> | 1.3 | 1347 | 37 | W81506 | IBDV VP2-VP3-VP4 poly <th>2.35e+02</th> | 2.35e+02 |
| 45 <td>1.3</td> <td>2482</td> <td>14</td> <td>R72826</td> <td>Long form of TPR moti<th>2.35e+02</th></td> | 1.3 | 2482 | 14 | R72826 | Long form of TPR moti <th>2.35e+02</th> | 2.35e+02 |
| | | | | | Human mitotin. | 2.35e+02 |

ALIGNMENTS

| RESULT | 1 | ALIGNMENTS |
|-----------------------|---|------------|
| ID | R60499 standard; Protein; 446 AA. | |
| AC | R60499; | |
| DT | 28-MAR-1995 (first entry) | |
| DE | linoleic-acid-desaturase; fadd; transgenic plant; crop improvement; | |
| KW | linoleic-acid-desaturase; fadd; transgenic plant; crop improvement; | |
| KW | linoleic acid. | |
| OS | Arabidopsis. | |
| PN | W09418337-A. | |
| PD | 18-AUG-1994. | |
| PF | 04-FEB-1994; U01321. | |
| PR | 05-NOV-1993; US-014431. | |
| PR | 22-NOV-1993; US-156551. | |
| PA | (MONS) MONSANTO CO. | |
| PA | (UNMS) UNIV MICHIGAN STATE. | |
| PI | Arandel VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR; | |
| DR | WPI: 94-279758/34. | |
| DR | N-PSDB; 071210. | |
| PT | Genetically transformed plants with altered linoleic acid | |
| PT | content - contg recombinant, double-stranded DNA encoding | |
| PT | linoleic acid desaturase, or the antisense of the coding | |
| PT | sequence | |
| PS | Disclosure: Page 75-77; 144pp; English. | |
| CC | The cDNA sequence and deduced amino acid sequence of linoleic- | |
| CC | acid-desaturase fadd of Arabidopsis are provided. | |
| CC | Sequence 446 AA; | |
| SQ | | |
| Query Match | 100.0%; Score 446; DB 11; Length 446; | |
| Best Local Similarity | 100.0%; Pred. No. 0.00e+00; | |
| Matches | 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Db | 1 manlvsecgirpripriytpirsnflsnmkffpslsssyktspslsglnsrdgfr 60 | |
| Qy | 1 MANLVSECGIRPLRITYTPRISNLFNNKFRSLSSSYKTSPPSLSGLNROGFT 60 | |
| Db | 61 nvalnvstpltpifesspleadkqgfdpgappfinaaiaipkhwvknpxksly 120 | |
| Qy | 61 NVALNVSTPLTPIFESSPLEEDNKORFDPGAPPFIMADIRAIPIKHCWKNPKWSLSY 120 | |
| Db | 121 vrvdvalvfaaagaaylnmvlwplywlaqgmfwalfvgndcgngstndpkinsv 180 | |

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|||||
QY 121 VVRDVAIVFALAAAGAAIYNMIVWPLYLWLAOGTFMFLFVGHDCGHSFSDNPKLSNV 180
Db 181 ghllhssilvpyhgwvshrtbhqbnghvendeswhpmseklynltdkptcffffftlply 240
QY 181 GHLHSSILVPHGWKRISHRTNHNHGHVENDSWHMPSEKITYNTLDKPTCFRFTPLV 240
Db 241 mlaypfylwarspgkshyhpdsdlfipkerkdvltstacwtamaallvcnlftgpiq 300
QY 241 MLAPFYLWARSpgKSHYHPDSDLFIPKERKDVLTSTACWTAMAALLVCNLTFTGPIQ 300
Db 301 mlklygipywlnvmwldfvcylhhghgedklpywrgkewsylyrglftldtgyllninh 360
QY 301 MLKLYGIPYWLNMWLDVYTLNHNHGHEDKLPWYRGKESWYLYRGSLTLDYGLINNIIH 360
Db 361 hdiqthvlnhlfpglpyhhlveateaakrvlgkyrpdksqgpljlllelaksikedh 420
QY 361 HDIGTHVNLHLPGLPYHHLVEATEAKRPVLGKYRPPDKSGPLJLHLEILAKSIKEDH 420
Db 421 yvsdegevvykkadpnllygekvkrad 446
QY 421 YVSDGEVYVYKKADPNLYGEVKVRAD 446
```

RESULT 2
ID R37593 standard; Protein; 446 AA.
AC R37593;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43204.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 132-134; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show overall homology of approx.
CC 80%.

SO Sequence 446 AA;
Query Match 100.0%; Score 446; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 1 manlvsecgtrpripftrftrnflnnnkfrpslssssyktsspslfnarqdftr 60
|||
QY 1 MANLVSECGRIPRIPFTRFTRNFLNNKFRPSLSSSSYKTSSPSLFGNLSDDGTR 60
|||
Db 61 nvalnvstpltpifseespleednkqrfdpgappfnadiiraalpkhckwknpkxslsy 120
|||
QY 61 NVALNVSTPLTPIFSEESPLEEDNKNQRFDPGAPPFNADIRAAIPKHCWKNPKXSLSY 120
|||
```

```
Db 121 vvrtaivafalaagaaylmmvlywplylwlaqgtcfnvalfvlghdcghgsfsndcklnsv 180
|||
QY 121 VVRDVAIVFALAAAGAAIYNMIVWPLYLWLAOGTFMFLFVGHDCGHSFSDNPKLSNV 180
Db 181 ghllhssilvpyhgwvshrtbhqbnghvendeswhpmseklynltdkptcffffftlply 240
QY 181 GHLHSSILVPHGWKRISHRTNHNHGHVENDSWHMPSEKITYNTLDKPTCFRFTPLV 240
Db 241 mlaypfylwarspgkshyhpdsdlfipkerkdvltstacwtamaallvcnlftgpiq 300
QY 241 MLAPFYLWARSpgKSHYHPDSDLFIPKERKDVLTSTACWTAMAALLVCNLTFTGPIQ 300
Db 301 mlklygipywlnvmwldfvcylhhghgedklpywrgkewsylyrglftldtgyllninh 360
QY 301 MLKLYGIPYWLNMWLDVYTLNHNHGHEDKLPWYRGKESWYLYRGSLTLDYGLINNIIH 360
Db 361 hdiqthvlnhlfpglpyhhlveateaakrvlgkyrpdksqgpljlllelaksikedh 420
QY 361 HDIGTHVNLHLPGLPYHHLVEATEAKRPVLGKYRPPDKSGPLJLHLEILAKSIKEDH 420
Db 421 yvsdegevvykkadpnllygekvkrad 446
QY 421 YVSDGEVYVYKKADPNLYGEVKVRAD 446
```

RESULT 3
ID R37591 standard; Protein; 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF3-f2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43205.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 136-138; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.

SO Sequence 378 AA;
Query Match 23.1%; Score 103; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.98e-162;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Db 239 lpyuinvmwldfvcylhhghgedklpywrgkewsylyrglftldtgyllninhidgth 298
|||
QY 307 IPYUINVMWLDVYTLNHNHGHEDKLPWYRGKESWYLYRGSLTLDYGLINNIIHIDIGTH 366
|||
Db 299 vlnhlfpglpyhhlveateaakrvlgkyrpdksqgpljll 341
|||
QY 367 VINHLFPGLPYHHLVEATEAKRPVLGKYRPPDKSGPLJLHL 409
|||
```

RESULT 4
ID R37594 standard; Protein; 404 AA.
AC R37594;
DT 01-OCT-1993 (first entry)
DE Sequence of plastid delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSFd-2.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR N-PSDB; 043206.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
fragment containing wild-type genomic DNA as a radiolabeled
hybridization probe. One of the sequencing primers made to the PCF3
insert was also used. The identity of the expression product of PCF3
as the Arabidopsis microsomal delta-15 desaturase was confirmed by
its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSFd-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA:

Query Match 23.1%; Score 103; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 2,98e-162;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 265 lpyvlnvwmvdfvylhghghedklpwrgkewylrgltldrdyglinnhldgth 324
|||||
QY 307 lpyvlnvwmvdfvylhghghedklpwrgkewylrgltldrdyglinnhldgth 366
|||||
QY 367 vihhlfpgihphylveateakpvlgykyrepdksgrplhll 367
|||||
QY 367 vihhlfpgihphylveateakpvlgykyrepdksgrplhll 409
|||||

RESULT 5
ID R60500 standard; Protein; 435 AA.
AC R60500;
DT 28-MAR-1995 (first entry)
DE linoletic-acid-desaturase; fade.
KW linoletic-acid-desaturase; fade; transgenic plant; crop improvement;
OS linoletic acid.
OS Arabidopsis.
PN M09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PI (UNMS) UNITV MICHIGAN STATE.
PI Atondel VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR,
DR WPI; 94-279758/34.
DR N-PSDB; Q71311.
PT Genetically transformed plants with altered linoletic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144pp; English.

CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fade of Arabidopsis are provided.
SQ Sequence 435 AA:

Query Match 9.6%; Score 43; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.59e-36;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 lnnhldgthvlnhlfpgihphylveateakpvlgykyrep 391
|||||
QY 356 lnnhldgthvlnhlfpgihphylveateakpvlgykyrep 398
|||||

RESULT 6
ID W13381 standard; Protein; 447 AA.
AC W13381;
DT 02-DEC-1997 (first entry)
DE Sesame omega-3 alphabetic acid desaturase.
KW Sesame; omega-3 alphabetic acid desaturase; modify; fat; oil; plant;
KW linoletic acid; recombinant production.
OS Sesamum indicum.
PN J09058883-A.
PD 11-MAR-1997.
PF 01-SEP-1995; 225145.
PR 01-SEP-1995; JP-225145.
PA (TOYA-) TOYAMA KEN.
DR WPI; 97-220417/20.
DR N-PSDB; T62066.
PT Sesame omega-3 alphabetic acid desaturase gene - useful in genetic
PT engineering to modify fats and oils in agricultural products
PS Claim 6; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 alphabetic acid desaturase. Its coding
CC sequence can be used in genetic engineering to modify fats and oils in
CC agricultural products. The gene or enzyme can be introduced into a plant
CC to modify the alphabetic acid composition in its oils and fats, to give
CC oils and fats with a high content of linoletic acid. Antisense DNA can
CC be introduced into a plant to inhibit the expression of the gene, so
CC that oils and fats with little or no linoletic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.
SQ Sequence 447 AA:

Query Match 8.1%; Score 36; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 1.46e-44;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 vtylhhghghedklpwrgkewylrgltldrdygl 358
|||||
QY 319 vtylhhghghedklpwrgkewylrgltldrdygl 354
|||||

RESULT 7
ID R37596 standard; Protein; 453 AA.
AC R37596;
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pSPD-118bp.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43208.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 148-150; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III

CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate a
 CC glycerolipid desaturase cDNA from soybean. Plasmid pXFI was
 CC deposited under ATCC 68874. Soybean microsomal delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
 CC encoding related desaturases from soybean. The insert of
 CC pSPD-118bp contained a stretch of 1675 nucleotides which contained
 CC an open-reading frame encoding a polypeptide (R37596) of about
 CC 80k identity with, and colinear with, the Arabidopsis plastid
 CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
 CC to 382 encode the putative plastid transit peptide, colinear with
 CC and sharing some homology with the transit peptide described for
 CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
 SQ Sequence 453 AA;

Query Match 8.1%; Score 36; DB 7; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1,46e-44;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 vtylhhbcklpyrgkewylgtltldryg 362
 |||||||
 Qy 319 VTYLHHGHEDKLPWYRGKESYLRGLTLDROYG 354

RESULT 8
 ID R37598 standard; Protein; 156 AA.
 AC R37598;
 DT 01-OCR-1993 (first entry)
 DE Sequence of a plastid delta-15 fatty acid.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pRadx-2 and pRadcp7.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43210.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 155; 167pp; English.
 CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
 CC composite sequence derived from the inserts in plasmids pRadx-2 and
 CC pRadcp7. R37598 is a deduced partial peptide sequence of its ORF.
 SQ Sequence 156 AA;

Query Match 6.5%; Score 29; DB 7; Length 156;
 Best Local Similarity 100.0%; Pred. No. 8,60e-33;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 rfdbpappfladlraaiphkwknpw 60
 |||||||
 Qy 87 RFDPGAPPPFNLADIRAIPIKHCWKWKNPM 115

RESULT 9
 ID R60498 standard; Protein; 383 AA.
 AC R60498;
 DT 28-MAR-1995 (first entry)
 DE Linoleic-acid-desaturase fad3
 KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
 KW transgenic plant; crop improvement; yeast artificial chromosome;
 KW YAC; linoleic acid.
 OS Brassica napus.
 PN W09418337-A.
 PD 18-AUG-1994.
 PF 04-FEB-1994; U01321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Aronow J, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
 DR WPI: 94-279758/34.
 DR N-PSDB: Q71203.
 PT Genetically transformed plants with altered linoleic acid
 PT content - contg recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence
 PS Disclosure; Page 69-71; 144pp; English.
 CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
 CC isolated from a YAC library using RFLP 220 and ASA2 markers as
 CC probes. Isolated DNA was amplified using the primers given in
 CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
 CC identified in YAC EW7D11.
 SQ Sequence 383 AA;

Query Match 6.3%; Score 28; DB 11; Length 383;
 Best Local Similarity 100.0%; Pred. No. 3,94e-31;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 llvpyghrshrhqnhghvdesw 150
 |||||||
 Qy 188 ILVPHGMRISRTHQHNGHVENDESM 215

RESULT 10
 ID R37592 standard; Protein; 386 AA.
 AC R37592;
 DT 01-OCR-1993 (first entry)
 DE Sequence of delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone pCF3.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43202.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 127-129; 167pp; English.
 CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224.
 SQ Sequence 386 AA;

| | Query Match | 6.3% | Score 28 | DB 7 | Length 386 |
|---------|---------------------------|---------------------------|-----------|------------|------------|
| | Best Local Similarity | 100.0% | Pred. NO. | 3.94e-31 | |
| Matches | 28 | Conservative | 0 | Mismatches | 0 |
| | | | | Indels | 0 |
| | | | | Gaps | 0 |
| Db | 11p9ytwr1shrtbqnhgvendesw | 153 | | | |
| | | | | | |
| Oy | 188 | 11p9ytwr1shrtbqnhgvendesw | 215 | | |

```

RESULT 11
ID R37595 standard; Protein; 380 AA.
AC R37595;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pXFI.
PN M03J11245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43207.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 144-146; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXFI was
CC deposited under ATCC 68874.
SC Sequence 380 AA;

Query Match 6.1%; Score 27; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.78e-29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 nhhdigfghvnhlfqgphvhyeat 321
OY 358 NHHDIGFHVHHLFPQIPHYHLVEAT 384

RESULT 12
ID R37597 standard; Protein; 126 AA.
AC R37597;
DT 01-OCT-1993 (first entry)
DE Sequence of an internal region of a corn seed delta-15
DE desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Zea mays, clone pPCR20.
PN M03J11245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43209.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to

```

PT specific polypeptide
PS Disclosure: Page 152-153; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the sequencing primers made to the PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43209 is the
CC complete nucleotide sequence of a 396 bp polymerase chain reaction
CC product derived from corn seed mRNA that is found in the insert of
CC plasmid pPCR80. Nucleotides 1 to 31 and 364 to 396 correspond to
CC the amplification primers described in Q43211 and Q43222
CC respectively. Nucleotides 31 to 363 encode a region that is 61.9%
CC identical to the region between amino acids 137 and 249 of R37591.
S0 Sequence 126 AA;

```

RESULT      13
ID          R80294 standard; Protein; 20 AA.
AC          R80294.
DE          19-JAN-1996 (first entry)
DT          trehalose releasing enzyme N-terminal fragment.
KW          Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW          alpha-maltotriosyltrehalose; alpha-maltotetraosyltrehalose;
KW          maltobiosyltrehalose; sweetener; taste-improving agent;
KW          stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW          pharmaceuticals.
OS          Arthrobacter sp. Q36.
PN          EP-671470-A2.
PD          13-SEP-1995.
PF          07-MAR-1995; 301474.
PR          07-MAR-1994; JP-059840.
PR          07-MAR-1994; JP-059834.
PA          (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
PI          Hattori K, Kubota M, Sugimoto T, Tsusaki K;
PI          WPI; 95-312772/41.
PT          DNA encoding a trehalose releasing enzyme - which releases trehalose
PT          from a non-reducing saccharide having a trehalose structure as an
PT          end unit.
PS          Example 4; Page 25; 45pp; English.
CC          The trehalose releasing enzyme can be used for the preparation of
CC          trehalose with high yields and efficiency from non-reducing
CC          saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC          alpha-maltotriosyltrehalose, alpha-maltotetraosyltrehalose and
CC          maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC          taste-improving agent, quality-improving agent, stabiliser, filler,
CC          excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC          This is the N-terminal sequence of the enzyme.
SQ          Sequence      20 AA;

Query Match      1.8%; Score 8; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.46e+00;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Db          7 eaakpvlg 14
          |||||
          |||||
Oy          385 EAAKPVLG 392

RESULT      14
ID          R80290 standard; Protein; 597 AA.
AC          R80290;

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| | |
|--------|----------------------------------|
| RESULT | 14 |
| ID | R80290 standard; Protein; 597 AA |
| AC | R80290; |

DT 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98670.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Claim 3; Page 24-25; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriose, alpha-maltotetraose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 597 AA;

Query Match 1.8%; Score 8; DB 14; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.46e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 eaakpvlg 14
|||||||
QY 385 ERAKPVLG 392

RESULT 15
ID R77471 standard; Protein; 598 AA.
AC R77471.
DT 25-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriose; alpha-maltotetraose; alpha-maltopentaose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Archaeobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98672.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
PT from a non-reducing saccharide having a trehalose structure as an
PT end unit.
PS Claim 6; Page 27-29; 45pp; English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriose, alpha-maltotetraose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 598 AA;

Query Match 1.8%; Score 8; DB 14; Length 598;

Best Local Similarity 100.0%; Pred. No. 1.46e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 8 eaakpvlg 15
|||||||
QY 385 ERAKPVLG 392

Search completed: Sat Aug 21 12:10:19 1999
Job time : 222 secs.

| | | | |
|-----------------------|--|--|-----|
| Db | 267 | YVWVMMLDVTVLHHNHGHEDEKIPWRKGKESNYLIRGGTLTDDRDYGLINNHHIDIGTVI | 326 |
| Oy | 241 | YVWVMMLDVTVLHHNHGHEDKIPWRKGKESYLIRGGTLTDDRQYGLINNNHHDIGTVI | 300 |
| Db | 327 | HHLFPGIPHNLVEATEAKPVLGVKKYYRPPDKSGPLPHLGILAKSKIEDHFVSDEGDV | 386 |
| Oy | 301 | HHLFPGIPHNLVEATEAKPVLGVKKYYRPPDKSGPLPHLGILAKSKIEDHFVSDEGDV | 360 |
| Db | 387 | VYEADPNLYGEIKVTAE | 404 |
| Oy | 361 | VYEADPNLYGEIKVTAE | 378 |
| RESULT | 2 | | |
| ENTRY | JQ2336 | #type complete | |
| TITLE | omega-3 fatty acid desaturase (EC 1.14.99.-) CFD - Arabidopsis thaliana | | |
| ORGANISM | #formal_name Arabidopsis thaliana #common_name mouse-ear cress | | |
| DATE | 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999 | | |
| ACCESSIONS | JQ2336; A49503 | | |
| REFERENCE | Yadav, N.S.; Wierzbicki, A.; Aegeerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schneider, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.T.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browne, J. | | |
| #journal | Plant Physiol. (1993) 103:467-476 | | |
| #title | Cloning of higher plant omega-3 fatty acid desaturases. | | |
| #cross-references | MJID:94302147 | | |
| #accession | JQ2336 | | |
| #molecule-type | mRNA | | |
| #residues | 1-446 ##label YAD | | |
| REFERENCE | A49503 | | |
| #authors | Ibb, K.; Gibson, S.; Nishituchi, T.; Fuse, T.; Nishimura, M.; Arondel, V.; Hugly, S.; Somerville, C. | | |
| #journal | J. Biol. Chem. (1993) 268:24099-24105 | | |
| #title | A gene encoding a chloroplast omega-3 fatty acid desaturase complements alterations in fatty acid desaturation and chloroplast copy number of the fad7 mutant of Arabidopsis thaliana. | | |
| #cross-references | MJID:94043239 | | |
| #accession | A49503 | | |
| #status | Preliminary | | |
| #molecule-type | DNA | | |
| #residues | 1-446 ##label IBA | | |
| #cross-references | GB:D14007; NID:g9461160; PID:d1003612; PID:g541653 | | |
| #note | sequence extracted from NCBI backbone (NCBIN:139485, NCBI:P139486) | | |
| COMMENT | The omega-6 and omega-3 fatty acid desaturases introduce the second and the third double bonds, respectively, in the biosynthesis of 18:2 and 18:3 fatty acids, which are important constituents of plant membranes. | | |
| CLASSIFICATION | #superfamily omega-3 fatty acid desaturase oxidoreductase | | |
| KEYWORDS | #length 446 #molecular-weight 51174 #checksum 4653 | | |
| SUMMARY | | | |
| Query Match | 27.2%; Score 103; DB 2; Length 446; | | |
| Best local Similarity | 100.0%; Pred. No. 4.62e-298; | | |
| Matches | 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| Db | 307 | IPWINNMMLDFPTVLHHNHGHEDKLPMWYGKESYLRGSLTLLDRDYGLINNHHIDIGH | 366 |
| Oy | 239 | IPWINNMMLDFPTVLHHNHGHEDKLPMWYGKESYLRGSLTLLDRDYGLINNHHIDIGH | 298 |
| Db | 367 | VIHHLFGPIRHNLVEATEAKPVLLGVKKYYRPPDKSGPLPHLH | 409 |
| Oy | 299 | VIHHLFGPIRHNLVEATEAKPVLLGVKKYYRPPDKSGPLPHLH | 341 |
| RESULT | 3 | | |

| | | |
|--|--|----------------|
| ENTRY | T01696 | #type fragment |
| TITLE | omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize | |
| ORGANISM | omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize (fragment) | |
| DATE | 19-Feb-1999 | |
| ACCESSIONS | #formal_name Zea mays #common_name maize | |
| REFERENCE | 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change | |
| #authors | T01696 | |
| #journal | 214400 | |
| #title | Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T. | |
| #accession | Plant Mol. Biol. (1998) 36:297-306 | |
| #status | Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature. | |
| ##molecule_type mRNA | T01696 | |
| ##residues | preliminary; translated from GB/EMBL/DBJ | |
| ##cross-references EMBL:D63953; NID:d1164452; PID:d1023305 | | |
| #experimental_source strain honey bantum | | |
| GENETICS | | |
| #gene | FAD8 | |
| KEYWORDS | oxidoreductase | |
| SUMMARY | #length 398 #checksum 5580 | |
| Query Match | 11.4%; Score 43; DB 2; Length 398; | |
| Best Local Similarity | 100.0%; Pred. No. 2.62e-102; | |
| Matches | 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Db | 291 EMSYLRGGLTTLDRDYLNNHHHDGTHYHHLFQIPHYHL 333 | |
| Qy | 270 EMSYLRGGLTTIDRDYGLNNHHHDGTHYHHLFQIPHYHL 312 | |
| RESULT | 4 | |
| ENTRY | T03029 | |
| TITLE | omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common tobacco | |
| ORGANISM | #formal_name Nicotiana tabacum #common_name common tobacco | |
| DATE | 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change | |
| ACCESSIONS | T03029 | |
| REFERENCE | 214828 | |
| #authors | Hanada, T.; Nishituchi, T.; Kodama, H.; Nishimura, M.; Iba, K. | |
| #journal | Plant Cell Physiol. (1996) 37:606-611 | |
| #title | CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid desaturase from tobacco. | |
| #accession | T03029 | |
| #status | preliminary; translated from GB/EMBL/DBJ | |
| ##molecule_type mRNA | | |
| ##residues | 1-441 ##label HAM | |
| ##cross-references EMBL:D79979; NID:d1093316; PID:g1694625 | | |
| #experimental_source cultivar SRL | | |
| GENETICS | | |
| #gene | FAD7 | |
| CLASSIFICATION | #superfamily omega-3 fatty acid desaturase | |
| KEYWORDS | oxidoreductase | |
| SUMMARY | #length 441 #molecular_weight 50310 #checksum 6941 | |
| Query Match | 10.6%; Score 40; DB 2; Length 441; | |
| Best Local Similarity | 100.0%; Pred. No. 7.29e-93; | |
| Matches | 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| Db | 355 INNIHHDIGTFVHHLFQIPHYHVEATFAAPVGLKYY 394 | |
| Qy | 288 INNIHHDIGTFVHHLFQIPHYHVEATFAAPVGLKYY 327 | |
| RESULT | 5 | |
| ENTRY | T01697 | |
| TITLE | omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize | |
| ORGANISM | #formal_name Zea mays #common_name maize | |
| DATE | 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change | |

ACCESSIONS T01697
REFERENCE B214400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.; Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and their differential expression to temperature.
#accession T01697
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 #label BBR
#cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantum

GENETICS
#gene FAD7
#introns 163/2: 193/2: 215/3: 246/3: 308/3: 335/3: 381/3
#exons oxidoreductase
#length 443 #molecular-weight 49437 #checksum 8872

KEYWORDS
SUMMARY

Query Match 9.5%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 2,23e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 352
|||
QY 251 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 286

RESULT 6
ENTRY JQ2339
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
#formal_name Glycine max #common_name soybean
#organism 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2339
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
#molecule_type mRNA
#residues 1-453 #label YAD
#cross-references GB:L22965; NID:9408791; PID:9408792

COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 9.5%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2,23e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 362
|||
QY 251 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 286

RESULT 7
ENTRY JQ2337
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BNS - rape
#formal_name Brassica napus #common_name rape
#organism 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.; Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.; Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.; Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.; Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BNS
#accession JQ2337
#molecule_type mRNA
#residues 1-377 #label YAD
#cross-references GB:L22962; NID:9408491; PID:9408492

COMMENT This enzyme introduces the third double bond in the biosynthesis of 18:2 and 18:3 fatty acids which are important constituents of plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 7.4%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.87e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVPHGWRISHRTHONHGHVDESM 144
|||
QY 120 ILVPHGWRISHRTHONHGHVDESM 147

RESULT 8
ENTRY A44227
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
#formal_name Brassica napus #common_name rape
#organism 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Aronde, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
#status Preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-383 #label ARO
#cross-references GB:L01418; NID:9167147; PID:9167148

COMMENT #experimental_source developing seed
#note Sequence extracted from NCBI backbone (NCBI:P119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 7.4%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 6.87e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGWRISHRTHONHGHVDESM 150
|||
QY 120 ILVPHGWRISHRTHONHGHVDESM 147

RESULT 9
ENTRY JQ2335
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear cress
#organism 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 12-Mar-1999

ACCESSIONS JQ2335
REFERENCE T02487

```

REFERENCE
#authors      Yadav, N.S.; Wierzbicki, A.; Aegeerter, M.; Caster, C.S.;
              Perce-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
              Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
              Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
              Pierce, J.; Browse, J.
#journal      Plant Physiol. (1993) 103:467-476
#title        Cloning of higher plant omega-3 fatty acid desaturases.
#citations    #cross-references MWID:94302147
#accession    JO2335
               ##molecule-type mRNA
               ##residues      1-386 ##label YAD
REFERENCE
#authors      Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
              Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
              J.C.;
              Ravelange, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
              J.C.
#submission   submitted to the EMBL Data Library, August 1998
#description   Arabidopsis thaliana chromosome II BAC F23f1 genomic
               sequence.
#accession     TO2487
               ##status
               ##molecule-type DNA
               ##residues      1-386 ##label ROU
CLASSIFICATION
KEYWORDS       #superfamily omega-3 fatty acid desaturase
               #oxidoreductase
SUMMARY         #length 386 #molecular-weight 44076 #checksum 8044

Query Match          7.4%; Score 28; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 6,87e-56;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVYHGWRISHRTHQNHGHVNDSEW 153
|||||HHHHHHHHHHHHHHHHHHHHHHH|||
QY 120 ILVYHGWRISHRTHQNHGHVNDSEW 147

RESULT 10
ENTRY   JO2338           #type complete
TITLE   omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE     30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
              17-Mar-1999
ACCESSIONS
ACCESSION JO2338
REFERENCE #authors      Yadav, N.S.; Wierzbicki, A.; Aegeerter, M.; Caster, C.S.;
              Perce-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
              Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
              Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
              Pierce, J.; Browse, J.
              #journal      Plant Physiol. (1993) 103:467-476
              #title        Cloning of higher plant omega-3 fatty acid desaturases.
              #citations    #cross-references MWID:94302147
              #accession    JO2338
               ##molecule-type mRNA
               ##residues      1-380 ##label YAD
COMMENT      The omega-6 and omega-3 fatty acid desaturases introduce the second
              and the third double bonds, respectively, in the biosynthesis of
              18:2 and 18:3 fatty acids, which are important constituents of
              plant membranes.
              #superfamily omega-3 fatty acid desaturase
              #oxidoreductase; Transmembrane protein
              #length 380 #molecular-weight 44185 #checksum 1659

```

| | | | | |
|-------------------|---|--------------------------------|----------------|---------------------------------|
| Query Match | 7.1% | Score 27 | DB 2 | Length 380 |
| Best Local | Similarity 100.0% | Pred. No. 6,90e-53 | | |
| Matches | 27 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0; |
| Db | 295 | NIHHDIGTHVHHLFPOIPHYHVEAT | 321 | |
| OY | 290 | NIHHDIGTHVHHLFPOIPHYHVEAT | 316 | |
| RESULT | 11 | | | |
| ENTRY | JC2555 | #type complete | | |
| TITLE | omega-3 fatty acid desaturase - common tobacco (cv. SR1) | | | |
| ORGANISM | #formal_name Nicotiana tabacum #common_name common tobacco | | | |
| DATE | 04-Sep-1998 | #sequence_revision 04-Sep-1998 | #text_change | |
| ACCESSIONS | JC2555 | | | |
| REFERENCE | JC2555 | | | |
| #authors | Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K. | | | |
| #journal | Gene (1994) 147:293-294 | | | |
| #title | Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase. | | | |
| #cross-references | MOLDB:95011632 | | | |
| #accession | JC2555 | | | |
| #status | preliminary | | | |
| #molecule_type | mRNA | | | |
| #residues | 1-379 | #label HAM | | |
| CLASSIFICATION | #cross-references DDBJ:D26509; NID:g1311480; PID:d1006059; PID:g5959522 | | | |
| SUMMARY | #superfamily omega-3 fatty acid desaturase | | | |
| | #length 379 | #molecular_weight 4419 | #checksum 1940 | |
| Query Match | 6.3% | Score 24 | DB 2 | Length 379 |
| Best Local | Similarity 100.0% | Pred. NO. 5.52e-44 | | |
| Matches | 24 | Conservative | 0 | Mismatches 0; Indels 0; Gaps 0; |
| Db | 291 | NIHHDIGTHVHHLFPOIPHYH | 314 | |
| OY | 289 | NIHHDIGTHVHHLFPOIPHYH | 312 | |
| RESULT | 12 | | | |
| ENTRY | S52650 | #type complete | | |
| TITLE | omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis | | | |
| ALTERNATE_NAMES | sp. (strain PCC6803) | | | |
| ORGANISM | delta 15 desaturase | | | |
| VARIETY | #formal_name Synechocystis sp. | | | |
| DATE | PCC 6803 | | | |
| | 28-Oct-1996 | #sequence_revision 13-Mar-1997 | #text_change | |
| ACCESSIONS | S52650 | | | |
| REFERENCE | S52649 | | | |
| #authors | Sakamoto, T.; Ios, D.A.; Higashi, S.; Wada, H.; Nishida, I.; | | | |
| #journal | Ohmori, M.; Murata, N. | | | |
| #title | Plant Mol. Biol. (1994) 26:249-263 | | | |
| | Cloning of omega-3 desaturase from cyanobacteria and its use | | | |
| | in altering the degree of membrane lipid unsaturation. | | | |
| #cross-references | MOLDB:95035996 | | | |
| #accession | S52650 | | | |
| #molecule_type | DNA | | | |
| #residues | 1-359 | #label SAK | | |
| #cross-references | GB:D13780; NID:g600596; PID:d1003430; PID:g600598 | | | |
| #note | the authors translated the initiation codon GTG for residue 1 as Val | | | |
| REFERENCE | S74322 | | | |
| #authors | Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; | | | |
| | Nakamura, Y.; Miyajima, N.; Hirosewa, M.; Sugitara, M.; | | | |
| | Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; | | | |
| | Murai, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpou, | | | |
| | S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; | | | |
| | Yasuda, M.; Tabata, S. | | | |
| | DNA Res. (1996) 3:109-136 | | | |
| | Sequence analysis of the genome of the unicellular | | | |
| | cyanobacterium Synechocystis sp. PCC6803. II. Sequence | | | |
| | determination of the entire genome and assignment of | | | |

potential protein-coding regions.

#cross-references MWID:97061201

#accession S75843

#status nucleic acid sequence not shown; translation not shown

#molecule-type DNA

#residues 1-359 #label KAN

#cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035; PID:g1653388

#note the nucleotide sequence was submitted to the EMBL Data Library, June 1996

GENETICS

#start_codon GTC

CLASSIFICATION

#superfamily omega-3 fatty acid desaturase oxidoreductase

SUMMARY

#length 359 #molecular-weight 41919 #checksum 9162

Query Match

Best Local Similarity 100.0%; Pred. No. 2,51e-21;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRISHRTH 129

114 ILVPHGWRISHRTH 129

120 ILVPHGWRISHRTH 135

RESULT 13

ENTRY H71349 #type complete

TITLE probable ribosomal protein L1 (rplA) - syphilis spirochete

ORGANISM #formal_name Treponema pallidum subsp. pallidum #common_name syphilis spirochete

DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999

ACCESSIONS H71349

REFERENCE A71250

#authors Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin, M.; Hickey, E.K.; Clayton, R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod, M.P.; Salzberg, S.; Petersen, J.; Khailak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utkerback, T.; McDonald, L.; Artach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.; Gairland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

#journal Science (1998) 281:375-388

#title Complete genome sequence of Treponema pallidum, the syphilis spirochete.

#cross-references MWID:98332770

#accession H71349

#status preliminary; nucleic acid sequence not shown; translation not shown

#molecule-type DNA

#residues 1-226 #label COL

#cross-references GB:AE001205; GB:AE000520; NID:g3322501; PID:g3322508

#experimental_source strain Nichols

GENETICS

#gene TP0238

CLASSIFICATION

#superfamily Escherichia coli ribosomal protein L1

SUMMARY

#length 226 #molecular-weight 24977 #checksum 6550

Query Match

Best Local Similarity 100.0%; Pred. No. 4.91e-02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAAGAY 90

83 ALAAGAY 90

62 ALAAGAY 69

RESULT 14

ENTRY S65770 #type complete

TITLE maltotigosyltrehalose trehalohydrolase - Arthrobacter sp. (strain Q36)

ORGANISM #formal_name Arthrobacter sp. #variety strain Q36

DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 18-Sep-1998

ACCESSIONS S65770

REFERENCE S65769

#authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto, T.; Kurimoto, M.

#journal Blochim. Biophys. Acta (1996) 1289:10-13

#title Cloning and sequencing of trehalose biosynthesis genes from Arthrobacter sp. Q36.

#cross-references MWID:96195835

#accession S65770

#status preliminary

#molecule-type DNA

#residues 1-598 #label MAR

#cross-references EMBL:D63343; NID:g1255444; PID:d1010313; PID:g1255446

CLASSIFICATION

#superfamily trehalose trehalohydrolase

SUMMARY

#length 598 #molecular-weight 65831 #checksum 4532

Query Match

Best Local Similarity 100.0%; Pred. No. 4.91e-02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAAKPYLG 15

8 EAAKPYLG 15

317 EAAKPYLG 324

RESULT 15

ENTRY S63399 #type complete

TITLE probable membrane protein YNR067c - yeast (Saccharomyces cerevisiae)

ALTERNATE_NAMES

ORGANISM #formal_name Saccharomyces cerevisiae

DATE 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 14-Nov-1997

ACCESSIONS S63399

REFERENCE S62944

#authors Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.

#submission submitted to the Protein Sequence Database, April 1996

#accession S63399

#molecule-type DNA

#residues 1-1117 #label DUE

#cross-references EMBL:D71682; NID:g1302597; PID:e239600; PID:g1302598; MIPS:YNR067c

#experimental_source strain S288c

GENETICS

#map_position 14R

KEYWORDS

FEATURE

6-22

SUMMARY

#domain transmembrane #status predicted #label TMM

#length 1117 #molecular-weight 121063 #checksum 7513

Query Match

Best Local Similarity 100.0%; Pred. No. 4.91e-02;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 339 TYDSSSP 346

339 TYDSSSP 346

2 TYDSSSP 9

Search completed: Sat Aug 21 12:24:17 1999

Job time : 60 secs.

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 (TM)

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Sat Aug 21 12:22:40 1999; Maspar time 11.12 Seconds
 Tabular output not generated. 961.326 Million cell updates/sec

Title: >US-09-219-935-7
 Description: (1-378) from US09219935.pep
 Perfect Score: 378
 Sequence: 1 LTVDSSSSPRIEERKQRF.....DVIYVYADPNLXGELKYAE 378

Scoring table: TABLE uniprottable
 Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot37
 1:swissprot

Statistics: Mean 3.703; Variance 0.432; scale 8.566

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------------------------------|-----------|
| 1 | 378 | 100.0 | 404 | 1 | FD3C_BRANA OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 2 | 103 | 27.2 | 446 | 1 | FD3C_ARATH OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 3 | 42 | 11.4 | 435 | 1 | FD3D_ARATH TEMPERATURE-SENSITIVE | 1.99e-110 |
| 4 | 42 | 11.1 | 460 | 1 | FD3C_RICCO OMEGA-3 FATTY ACID DES | 5.10e-107 |
| 5 | 36 | 9.5 | 447 | 1 | FD3C_SESIN OMEGA-3 FATTY ACID DES | 9.53e-87 |
| 6 | 36 | 9.5 | 453 | 1 | FD3C_SOYBN OMEGA-3 FATTY ACID DES | 9.53e-87 |
| 7 | 28 | 7.4 | 377 | 1 | FD31_BRANA OMEGA-3 FATTY ACID DES | 2.52e-60 |
| 8 | 28 | 7.4 | 383 | 1 | FD32_BRANA OMEGA-3 FATTY ACID DES | 2.52e-60 |
| 9 | 28 | 7.4 | 386 | 1 | FD3E_ARATH OMEGA-3 FATTY ACID DES | 2.52e-60 |
| 10 | 27 | 7.1 | 380 | 1 | FD3E_SOYBN OMEGA-3 FATTY ACID DES | 4.36e-57 |
| 11 | 25 | 6.6 | 380 | 1 | FD3E_PHAU OMEGA-3 FATTY ACID DES | 1.14e-50 |
| 12 | 24 | 6.3 | 379 | 1 | FD3E_TOBAC OMEGA-3 FATTY ACID DES | 1.73e-47 |
| 13 | 21 | 2.1 | 326 | 1 | RIL1_TREPA 50S RIBOSOMAL PROTEIN | 1.92e-02 |
| 14 | 8 | 2.1 | 1117 | 1 | YV96_YEAST HYPOTHETICAL 121.1 KD | 1.92e-02 |
| 15 | 7 | 1.9 | 85 | 1 | CH10_THERM 50S RIBOSOMAL PROTEIN | 1.86e+00 |
| 16 | 7 | 1.9 | 100 | 1 | AGN5_APLCA ABDOMINAL GANGLION NEU | 1.86e+00 |
| 17 | 7 | 1.9 | 143 | 1 | SYU_TORCA SYNUNCLIN | 1.86e+00 |
| 18 | 7 | 1.9 | 213 | 1 | LEAL_HORVU ABA-INDUCIBLE PROTEIN | 1.86e+00 |
| 19 | 7 | 1.9 | 232 | 1 | Y08E_MYCTU HYPOTHETICAL 23.9 KD P | 1.86e+00 |
| 20 | 7 | 1.9 | 236 | 1 | LYSE_CORNL LYSINE EXPORTER PROTEIN | 1.86e+00 |
| 21 | 7 | 1.9 | 280 | 1 | DUS7_RAT DUAL SPECIFICITY PROTE | 1.86e+00 |
| 22 | 7 | 1.9 | 322 | 1 | DUS7_HUMAN DUAL SPECIFICITY PROTE | 1.86e+00 |
| 23 | 7 | 1.9 | 322 | 1 | DUS7_HUMAN DUAL SPECIFICITY PROTE | 1.86e+00 |

| | | | | | | |
|----|---|-----|------|---|-----------------------------------|----------|
| 24 | 7 | 1.9 | 336 | 1 | PTLS_STRSQ PENTALENE SYNTHASE (| 1.86e+00 |
| 25 | 7 | 1.9 | 367 | 1 | A2HS_HUMAN ALPHA-2-HS-GLYCOPROTEI | 1.86e+00 |
| 26 | 7 | 1.9 | 388 | 1 | ALR_MYCLE ALANINE RACEMASE (EC 5 | 1.86e+00 |
| 27 | 7 | 1.9 | 389 | 1 | ALR_MYCSM ALANINE RACEMASE (EC 5 | 1.86e+00 |
| 28 | 7 | 1.9 | 392 | 1 | EAST_DROME SERINE PROTEASE EASTER | 1.86e+00 |
| 29 | 7 | 1.9 | 415 | 1 | SAHH_METJA ADENOSYLHOMOCYSTEINASE | 1.86e+00 |
| 30 | 7 | 1.9 | 417 | 1 | RBL_ACRAU RIBULOSE BIPHOSPHATE | 1.86e+00 |
| 31 | 7 | 1.9 | 447 | 1 | YF66_METJA HYPOTHETICAL PROTEIN M | 1.86e+00 |
| 32 | 7 | 1.9 | 470 | 1 | EZF_HUMAN EPITHELIAL ZINC-FINGER | 1.86e+00 |
| 33 | 7 | 1.9 | 474 | 1 | EZF_MOUSE GUT ENRICHED KRUPPEL-L | 1.86e+00 |
| 34 | 7 | 1.9 | 488 | 1 | EXON_HSV6U ALKALINE EXONUCLEASE (| 1.86e+00 |
| 35 | 7 | 1.9 | 488 | 1 | EXON_HSV6Z ALKALINE EXONUCLEASE (| 1.86e+00 |
| 36 | 7 | 1.9 | 553 | 1 | C862_ARATH CYTOCHROME P450 86A2 (| 1.86e+00 |
| 37 | 7 | 1.9 | 555 | 1 | WEEL_XENLA WEEL-LIKE PROTEIN KINA | 1.86e+00 |
| 38 | 7 | 1.9 | 631 | 1 | O866_NPVIS OCCLUSION-DERIVED VIRU | 1.86e+00 |
| 39 | 7 | 1.9 | 1045 | 1 | Y052_HUMAN HYPOTHETICAL PROTEIN K | 1.86e+00 |
| 40 | 7 | 1.9 | 1132 | 1 | TKK5_YEAST HYPOTHETICAL 125.6 KD | 1.86e+00 |
| 41 | 7 | 1.9 | 1944 | 1 | TS24_MOUSE PROTEIN TS24 (MEIOTIC | 1.86e+00 |
| 42 | 7 | 1.9 | 2038 | 1 | FSH_DROME FEMALE STERILE HOMEOTI | 1.86e+00 |
| 43 | 7 | 1.9 | 2468 | 1 | MAPB_HUMAN MICROTUBULE-ASSOCIATED | 1.86e+00 |
| 44 | 6 | 1.6 | 253 | 1 | Y0YL_BACSU HYPOTHETICAL 28.2 KD P | 1.01e+02 |
| 45 | 6 | 1.6 | 534 | 1 | YH22_CAEBL HYPOTHETICAL 58.7 KD P | 1.01e+02 |

ALIGNMENTS

RESULT 1
 ID FD3C_BRANA STANDARD; PRT: 404 AA.
 AC P48618;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
 DE (FRAGMENT).
 GN FAD7.
 OS BRASSICA NAPUS (RAPE).
 OC EUKARYOTA: VIRIDIPHYTES: EMBRYOPHYTA: TRACHEOPHYTA:
 OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
 OC CAPRIFALES: BRASSICACEAE: BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE: 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWELGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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 or send an email to license@sib-sib.ch).
 CC
 DR EMBL: L22963; G408490; ALT_INIT.
 DR PIR: P00812; P00812.
 DR PFM: PFO0487; FA_desaturase; 1.
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 TRANSIT PEPTIDE.

```

FT  NON TER      1      1
FT  TRANSIT      <1      ?
FT  CHAIN        ?      404
FT  DOMAIN      121     125
FT  DOMAIN      157     161
FT  DOMAIN      324     328
SQ  SEQUENCE     404 AA; 46617 MW; 797F19FB CRC32;

Query Match      100.0%; Score 378; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  27  LTVSSSSPPIEEPKTQRFPGAPPPNLDIRAIRKHCWKVKNPKMSGYVRELAIY 86
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QY  1  LTVSSSSPPIEEPKTQRFPGAPPPNLDIRAIRKHCWKVKNPKMSGYVRELAIY 60

Db  87  FALAAGAYLNNWLVWPLWYIAOGTMMFALVGLHDCGHSFSDNPRNSVVGHLHSSI 146
    |||||
QY  61  FALAAGAYLNNWLVWPLWYIAOGTMMFALVGLHDCGHSFSDNPRNSVVGHLHSSI 120

Db  147  LVPYHGWRIISHRTIHQNHGVENDESMHPSSEKITYKSLDKPTREFRFTLPVLMALPYFL 206
    |||||
QY  121  LVPYHGWRIISHRTIHQNHGVENDESMHPSSEKITYKSLDKPTREFRFTLPVLMALPYFL 180

Db  207  WARSPPKGGSHYHPDSDLFLFKERNVLTSTACTATAVLLVCLNFVNGPMQMLKIYIP 266
    |||||
QY  181  WARSPPKGGSHYHPDSDLFLFKERNVLTSTACTATAVLLVCLNFVNGPMQMLKIYIP 240

Db  267  YWVNWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIDGTHVI 326
    |||||
QY  241  YWVNWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIDGTHVI 300

Db  327  HHLFPOIPHYHLVEATEAKPYLGYREPPKSGPLPLHLGLILAKSIKEDHFVSDGDV 386
    |||||
QY  301  HHLFPOIPHYHLVEATEAKPYLGYREPPKSGPLPLHLGLILAKSIKEDHFVSDGDV 360

Db  387  VYEADPNLYGEIKVTAE 404
    |||||
QY  361  VYEADPNLYGEIKVTAE 378

RESULT  2
ID  FD3D_ARATH  STANDARD;  PRT;  446 AA.
AC  P46310;
DT  01-NOV-1995 (REL. 32, CREATED)
DT  01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT  01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN  FAD7 OR FAD8.
OS  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC  CHLOROPLAST.
OC  EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC  EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE:
OC  CAPRALES; BRASSICACEAE; ARABIDOPSIS.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
RA  MEDLINE: 94032147.
RA  YDANV N.S., WIEZBICKI A., ASSEFTER M., CASTER C.S., PEREZ-GRAU L.,
RA  KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHMEIGER B., STECCA K.L.,
RA  ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA  FELDMAN N.K.A., PIERCE J., BROWSE J.;
RT  "Cloning of higher plant omega-3 fatty acid desaturases.";
RL  PLANT PHYSIOL. 103:467-476(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA; TISSUE=ARIAL PARTS;
RA  MEDLINE: 94043239.
RA  IBA K., GIBSON S., NISHIOUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA  HUGLY S., SOMERVILLE C.R.;
RT  "A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and chloroplast

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RT  copy number of the fad7 mutant of Arabidopsis thaliana.";
RL  J. Biol. Chem. 268:24099-24105(1993).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;
RA  WATABIKI M., YAMAMOTO K.;
RL  SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC  -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC  THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC  ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC  TO USE FERRODOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC  ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC  -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC  -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC  -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC  -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC  AND/OR BE INVOLVED IN METAL ION BINDING.
CC  -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
-----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; L22961; G408481; -
DR  EMBL; D14007; G541653; -
DR  EMBL; D26019; G468434; -
DR  PFM; P00487; FA_desaturase; 1.
KW  OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KT  TRANSIT PEPTIDE.
FT  TRANSIT 1
FT  CHAIN ? 446
FT  DOMAIN 163 167 CHLOROPLAST (POTENTIAL).
FT  DOMAIN 199 203 OMEGA-3 FATTY ACID DESATURASE,
FT  DOMAIN 366 370 HISTIDINE BOX 2.
SQ  SEQUENCE 446 AA; 51174 MW; 8DE08779 CRC32;

Query Match      27.2%; Score 103; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  307  IPYINWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIDGTH 366
    |||||
QY  239  IPYINWMLDEFTYLLHHGHEDKLPYRGKEMSYLRGSLTTLDRDYGILNNHHIDGTH 298

Db  367  VIHHLFPOIPHYHLVEATEAKPYLGYREPPKSGPLPLHL 409
    |||||
QY  299  VIHHLFPOIPHYHLVEATEAKPYLGYREPPKSGPLPLHL 341

RESULT  3
ID  FD3D_ARATH  STANDARD;  PRT;  435 AA.
AC  P48622;
DT  01-FEB-1996 (REL. 33, CREATED)
DT  01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT  01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE  TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE  PRECURSOR (EC 1.14.99.-).
GN  FAD8.
OS  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC  EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC  EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE:
OC  CAPRALES; BRASSICACEAE; ARABIDOPSIS.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=CV. COLUMBIA; TISSUE=ARIAL PARTS;
RA  MEDLINE: 95148742.
RA  GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT  "Cloning of a temperature-regulated gene encoding a chloroplast

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RT omega-3-desaturase from Arabidopsis thaliana", 1994).
RL PLANT PHYSIOL. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE=HYPOCOTYL.
RA WATAHAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@sib.ch).
CC -----
CC EMBL; L27158; G516045; -
CC DR EMBL; U08216; G497219; -
CC DR EMBL; D17578; G471093; -
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
CC TRANSIT PEPTIDE.
CC FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
CC FT CHAIN 1 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
CC FT FT DESATURASE, CHLOROPLAST.
CC FT DOMAIN 156 160 HISTIDINE BOX 1.
CC FT FT 192 196 HISTIDINE BOX 2.
CC FT DOMAIN 359 363 HISTIDINE BOX 3.
CC SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;

Query Match 11.4%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,99e-110;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHHIGTHVYHHLFPQIPHYHLYVEATEAKPYLGKXRRP 391
Oy 288 INNHHHIGTHVYHHLFPQIPHYHLYVEATEAKPYLGKXRRP 330

RESULT 4 STANDARD: PRT: 460 AA.
AC FD3C_RICCO
AC P48619;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
DE PAD7A-1.
GN RICINUS COMMUNIS (CASTOR BEAN).
OS EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMERYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
RN (1)
RN SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE=SEED;
RX MEDLINE: 94302177.
RA VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
CC CC PLANT PHYSIOL. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL; L27158; G516045; -
CC DR EMBL; U08216; G497219; -
CC DR EMBL; D17578; G471093; -
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
CC TRANSIT PEPTIDE.
CC FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
CC FT CHAIN 1 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
CC FT FT DESATURASE, CHLOROPLAST.
CC FT DOMAIN 156 160 HISTIDINE BOX 1.
CC FT FT 192 196 HISTIDINE BOX 2.
CC FT DOMAIN 359 363 HISTIDINE BOX 3.
CC SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;

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CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL; L25897; GA14732; -.
DR PFAM; PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT TRANSIT 1.
FT CHAIN ? ? CHLOROPLAST (POTENTIAL)
FT ? 460 OMEGA-3 FATTY ACID DESATURASE,
FT CHLOROPLAST.
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 280 384 HISTIDINE BOX 3.
SQ SEQUENCE 460 AA; 52561 MW; DB3DB689 CRC32;

Query Match 11.1%; Score 42; DB 1; Length 460;
Best Local Similarity 100.0%; Pred. No. 5,106-107;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 190 LNSVYGHLLHSILVPHYGWRISRTTHQNHGHVNDSEWHP 231
Qy 108 LNSVYGHLLHSILVPHYGWRISRTTHQNHGHVNDSEWHP 149
|||||
RESULT 5 STANDARD: PRT: 447 AA.
AC FD3C_SESIN
AC P46620;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
PRT:
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY).
OC EUPARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALIACEAE; SESAMUM.
OC [1]
RN SEQUENCE FROM N.A.
RP SHOUJ K.;
RC STRAIN-CV. 4294; TISSUE-COTYLEDON;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASES INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, PERMELOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL; U25817; G870784; -.
DR PFAM; PF00487; FA_desaturase; 1.

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KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE. 1.
 FT TRANSIT 1. ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 447 OMEGA-3 FATTY ACID DESATURASE,
 CHLOROPLAST.
 FT DOMAIN 167 171 HISTIDINE BOX 1.
 FT DOMAIN 203 207 HISTIDINE BOX 2.
 FT DOMAIN 370 374 HISTIDINE BOX 3.
 SQ SEQUENCE 447 AA; 5116 MW; 67B2C46B CRC32;

Query Match 9.5%; Score 36; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 9.53e-87;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 358
 251 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 286

RESULT 6
 ID PD3C_SOYBN STANDARD; PRT: 453 AA.
 AC P48621;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 GN FAD7.
 OS GLYCINE MAX (SOYBEAN).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE: 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHMEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMANN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASES."
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 CC EMBL: L22965; G408792; -.
 DR PRAM: PF00487; FA.desaturase; 1.
 DR PIR: JQ2339; JQ2339.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1. ?
 FT CHAIN ? 453 CHLOROPLAST (POTENTIAL).
 FT DOMAIN 171 175 HISTIDINE BOX 1.
 FT DOMAIN 207 211 HISTIDINE BOX 2.
 FT ~DOMAIN 374 378 HISTIDINE BOX 3.
 SQ SEQUENCE 453 AA; 51362 MW; E431AF1B CRC32;

Query Match 9.5%; Score 36; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 9.53e-87;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 362
 251 VTYLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYG 286

RESULT 7
 ID PD31_BRANA STANDARD; PRT: 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (VERSION 1).
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPALES; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE: 94302147.
 RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHMEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMANN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 CC EMBL: L22962; G408492; -.
 DR PRAM: PF00487; FA.desaturase; 1.
 DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 54 73 POTENTIAL.
 FT TRANSMEM 203 226 POTENTIAL.
 FT TRANSMEM 233 251 POTENTIAL.
 FT DOMAIN 92 96 HISTIDINE BOX 1.
 FT DOMAIN 128 132 HISTIDINE BOX 2.
 FT DOMAIN 295 299 HISTIDINE BOX 3.
 SQ SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;

Query Match 7.4%; Score 28; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.52e-60;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVYHGMRISHTRHONHGHVNDSE 144
 120 ILVYHGMRISHTRHONHGHVNDSE 147

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RESULT 8
ID FD32-BRANA STANDARD; PRT: 363 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUPHYLLOPHYTES: VIRIDIPANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
CAPPALES; BRASSICACEAE; BRASSICA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93080059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.*;
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L01418; G167148; -.
CC DR PRAM; PF00487; FA_desaturase; 1.
CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 53 73 POTENTIAL.
CC FT TRANSMEM 210 230 POTENTIAL.
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 98 102 HISTIDINE BOX 1.
CC FT DOMAIN 134 138 HISTIDINE BOX 2.
CC FT DOMAIN 301 305 HISTIDINE BOX 3.
CC SO SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;

Query Match 7.4%; Score 28; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 2,52e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVPHGMRIHRTTHQNHGVNDESM 150
OY 120 ILVPHGMRIHRTTHQNHGVNDESM 147

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OC CAPPALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA; TISSUE-SEEDLING;
RX MEDLINE: 94302147.
RA YADAV N.S., WIENZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases.*;
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA;
RX MEDLINE: 94345020.
RA NISHITUCHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.*;
RL PLANT PHYSIOL. 105:767-768(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA;
RA ROUNSELEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA STRES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., YENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L22931; G408483; -.
CC DR EMBL; D17579; G471091; -.
CC DR EMBL; D26508; G1197795; -.
CC DR EMBL; AC004680; G3420053; -.
CC PRAM; PF00487; FA_desaturase; 1.
CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 220 240 POTENTIAL.
CC FT TRANSMEM 242 262 POTENTIAL.
CC FT DOMAIN 101 105 HISTIDINE BOX 1.
CC FT DOMAIN 137 141 HISTIDINE BOX 2.
CC FT DOMAIN 304 308 HISTIDINE BOX 3.
CC SO SEQUENCE 386 AA; 44076 MW; C22B4B8C CRC32;

Query Match 7.4%; Score 28; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 2,52e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPHGMRIHRTTHQNHGVNDESM 153

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|||||
OY 120 ILVPHGMRISRTTHQNHGVNDESW 147

RESULT 10
ID FD3E_S0YBN STANDARD: PRT: 380 AA.
AC P48625:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS GLYCINE MAX (SOYBEAN).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES: FABACEAE: PAPILIONOIDEAE: GLYCINE.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SEED:
RX MEDLINE: 94302147.
RA YADAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FEIDMANN K.A., PIERCE J., BROWSE J.:
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L22964; J0408794; -.
DR PIR: J02338; J02338.
DR PFAM: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE: FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
FT SEQUENCE 380 AA: 44185 MW: E3C509B7 CRC32:

Query Match 7.1%; Score 27; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 4,36e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 295 NINHDIQTHVHHLFPOIPHYHLVEAT 321
OY 290 NINHDIQTHVHHLFPOIPHYHLVEAT 316

RESULT 11
ID FD3E_PHAU STANDARD: PRT: 380 AA.
AC P32291.
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
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DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
GN ARG1.
OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC FABALES: FABACEAE: PAPILIONOIDEAE: VIGNA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOCOTYL.
RX YAMAMOTO K.T., MORI H., IMASEKI H.:
RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
RT elongating hypocotyls of mung bean (Vigna radiata).".
RL PLANT CELL PHYSIOL. 33:13-20(1992).
CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: D14410; G287562; -.
DR PFAM: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE: FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 59 78 POTENTIAL.
FT TRANSMEM 208 231 POTENTIAL.
FT TRANSMEM 238 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
FT SEQUENCE 380 AA: 43996 MW: 8429BF68 CRC32:

Query Match 6.6%; Score 25; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.14e-50;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 294 HHDIGTHVHHLFPOIPHYHLVEAT 318
OY 292 HHDIGTHVHHLFPOIPHYHLVEAT 316

RESULT 12
ID FD3E_TOBAC STANDARD: PRT: 379 AA.
AC P48626:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS:
OC ASTERIDAE: SOLANACEAE: SOLANACEAE: SOLANACEAE: NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SRI; TISSUE=LEAF;
RX MEDLINE: 95011632.
```

RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.:
RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase."
RL GENE 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS.
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
CC EMBL: D36509; G599592; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 236 236 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;

Query Match 6.3%; Score 24; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.73e-47;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 291 NNTHDICTVHHLFPQIPHYHL 314
QY 289 NNTHDICTVHHLFPQIPHYHL 312

RESULT 13
ID RL1 TREPA STANDARD; PRT; 226 AA.
AC 083266;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DE 50S RIBOSOMAL PROTEIN L1.
GN RPLA OR TP0238.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDABARAM M., UTTERBACK T.,
RA McDONALD L., ARTSCH P., BOWMAN C., COTTON M.D., FUJII C., GARIAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL SCIENCE 281:375-388(1998).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.
CC

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CC
CC EMBL: AE001205; G3322508; -
DR TIGR: TP0238;
DR PROSITE: PS01199; RIBOSOMAL_L1; 1.
KW RIBOSOMAL PROTEIN; RNA-BINDING.
SQ SEQUENCE 226 AA; 24977 MW; 423DF8A1 CRC32;

Query Match 2.1%; Score 8; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 1.92e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 83 ALAAGAY 90
QY 62 ALAAGAY 69

RESULT 14
ID YN96_YEAST STANDARD; PRT; 1117 AA.
AC P53753;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION
DE PRECURSOR.
GN YNR067C OR N3547.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCYCETES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA DUESTERHOEFT A., FLOETH M., FRITZ C., HEUSS-NEITZEL D.,
RA HILBERT H., MOESTL D.,
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: TO YEAST YLR144C AND S.POMBE SPAC23D3.10C.
CC
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CC
CC EMBL: Z71682; E238600; -
DR HYPOTHEICAL PROTEIN; GLYCOPROTEIN; SIGNAL.
KW HYPOTHEICAL PROTEIN; SIGNAL.
FT SIGNAL 1 16
FT CHAIN 17 1117
FT DOMAIN 342 345
FT DOMAIN 365 370
FT DOMAIN 376 383
FT DOMAIN 138 138
FT CARBOHYD 186 186
FT CARBOHYD 223 223
FT CARBOHYD 223 223
FT CARBOHYD 259 259
FT CARBOHYD 280 280
FT CARBOHYD 303 303
FT CARBOHYD 307 307
FT CARBOHYD 333 333
FT CARBOHYD 533 533
FT CARBOHYD 866 886
SQ SEQUENCE 1117 AA; 121063 MW; 9AB486C6 CRC32;

Query Match 2.1%; Score 8; DB 1; Length 1117;
Best Local Similarity 100.0%; Pred. No. 1.92e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 339 TVDSSSP 346
 |||||
 OY 2 TVDSSSP 9

RESULT 15
 ID RU27_STRGR STANDARD: PRT: 85 AA.

AC P95757;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L27.

GN RPA.
 OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189;
 RX MEDLINE; 97136618.

RA OKAMOTO S., ITOH M., OCHI K.;
 RT "Molecular cloning and characterization of the obp gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation";

RL J. BACTERIOL. 179:170-179(1997).
 CC -1- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.

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 CC -----

DR EMBL: D87916; G1783293;
 DR PROSITE; PS00831; RIBOSOMAL_L27; 1.
 DR PIRAM; PF01016; Ribosomal_L27; 1.
 KW RIBOSOMAL PROTEIN.

SQ SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.9%; Score 7; DB 1; Length 85;
 Best Local Similarity 100.0%; Pred.No. 1.86e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAGA 66
 |||||
 OY 61 FALAGA 67

Search completed: Sat Aug 21 12:22:59 1999
 Job time : 19 secs.

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:24:34 1999; Maspar time 22.49 Seconds
Tabular output not generated.
Title: >US-09-219-935-7
Description: (1-378) from US09219935.pep
Perfect Score: 378
Sequence: 1 LTVDSSSSPRIEERKQRF.....DYYVEADPNLGEIKYTAE 378
Scoring table: TABLE uniprottable
Gap 60
Searched: 179066 seqs, 54579741 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: sptrembl9
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus
Statistics: Mean 3.602; Variance 0.446; scale 8.079
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES
Result No. Score Match Length DB ID Description Pred. No.
1 47 12.4 436 10 Q40118 DELTA-15 LINEOYL DESAT 1.69e-117
2 43 11.4 398 10 Q24626 FATTY ACID DESATURASE 1.52e-104
3 40 10.6 431 10 O82068 W-3 DESATURASE 6.72e-95
4 40 10.6 441 10 P93350 OMEGA-3 FATTY ACID DES 6.72e-95
5 37 9.8 438 10 O04807 OMEGA-3 FATTY ACID DES 2.54e-85
6 36 9.5 443 10 O23824 FATTY ACID DESATURASE 3.81e-82
7 34 9.0 438 10 P93452 OMEGA-3 FATTY ACID DES 8.01e-76
8 29 7.7 381 10 P94013 W-3 FATTY ACID DESATUR 3.27e-60
9 29 7.7 383 10 O65792 OMEGA-3 FATTY ACID DES 3.27e-60
10 28 7.4 407 10 O64907 OMEGA-3 DESATURASE (FR 3.96e-57
11 24 6.3 380 10 O23802 PLASTID OMEGA-3 FATTY 5.77e-45
12 16 4.2 359 2 O55240 DELTA-15 DESATURASE 8.34e-22
13 13 2.9 350 2 O07872 OMEGA-3 DESATURASE 8.89e-09
14 11 2.1 193 3 O24442 FATTY ACID DESATURASE 4.64e-02
15 8 2.1 598 2 O44316 MALTOOLIGOSYL TERPHAS 4.64e-02
16 8 2.1 4848 2 O07944 PRISTINAMICIN I SYNTHA 4.64e-02
17 7 1.9 92 10 P93687 REVERSE TRANSCRIPTASE 3.90e+00
18 7 1.9 224 10 O03968 LATE EMBRYOGENESIS ABU 3.90e+00
19 7 1.9 299 10 O80551 T22118.13 PROTEIN. 3.90e+00
20 7 1.9 305 2 O50934 CONSERVED HYPOTHETICAL 3.90e+00

ALIGNMENTS
RESULT 1
ID Q40118 PRELIMINARY; PRT; 436 AA.
AC Q40118;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE DELTA-15 LINEOYL DESATURASE.
OS LIMNANTHES DOUGLASSII.
OC EUKARYOTA: VIRIDIPHYTA: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPPALALES; LIMNANTHACEAE; LIMNANTHES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95334518.
RA BHEILA R.S., MACKENZIE S.L.;
RT "Nucleotide sequence of a cDNA from Limnantes douglasi L. encoding
a delta-15 linoleic acid desaturase.";
RL PLANT PHYSIOL. 108:861-861(1995).
DR EMBL: U17063; G699390; -.
DR PFM: PF00487; FA.desaturase; 1.
DR MENDEL, 8699; LIMDO:12081.
SQ SEQUENCE 436 AA: 50093 MW: 327077FE CRC32:
Query Match 12.4%; Score 47; DB 10; Length 436;
Best Local Similarity 100.0%; Pred. No. 1.69e-117;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 330 EWSLIRGLTLDRLDYLINNHHIDTGVYIHLEFPIPIHYHVEAT 376
QY 270 EWSYLIRGLTLDRLDYLINNHHIDTGVYIHLEFPIPIHYHVEAT 316
RESULT 2
ID Q24626 PRELIMINARY; PRT; 398 AA.
AC Q24626;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
GN FAD8.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA: VIRIDIPHYTA: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;
OC POACEAE; ZEA.

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RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -.
DR EMBL: D63953; D1023305; -.
DR PFM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565EEC CRC32;

Query Match 11.4%; Score 43; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1,52e-104;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGSLTLDRDYGILNNIHHDIGTHVHILFPQIPHYHL 333
Y 270 EMSYLRGSLTLDRDYGILNNIHHDIGTHVHILFPQIPHYHL 312

RESULT 3
ID 082068; PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ007739; E1318202; -.
SQ SEQUENCE 431 AA; 49253 MW; BAF9F9CD CRC32;

Query Match 10.6%; Score 40; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 6.72e-95;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 345 INNTHHDIGTHVHILFPQIPHYHLVEATEAKPVLGKYY 384
Y 288 INNTHHDIGTHVHILFPQIPHYHLVEATEAKPVLGKYY 327

RESULT 4
ID P93350; PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NFEAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 96416425.
RA HAMADA T., NISHITUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "cDNA cloning of a wounding-inducible gene encoding a plastid omega-3
fatty acid desaturase from tobacco.";
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL: D79979; D1012141; -.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;
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DR PFM: PF00487; FA_desaturase; 1.
DR MENDEL; 9312; NICIA;1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;

Query Match 10.6%; Score 40; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.72e-95;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNTHHDIGTHVHILFPQIPHYHLVEATEAKPVLGKYY 394
Y 288 INNTHHDIGTHVHILFPQIPHYHLVEATEAKPVLGKYY 327

RESULT 5
ID 004807; PRELIMINARY; PRT; 438 AA.
AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U58477; G1754795; -.
DR PFM: PF00487; FA_desaturase; 1.
DR MENDEL; 16268; PERIL;1208;mm16268.
SQ SEQUENCE 438 AA; 50160 MW; EE726819 CRC32;

Query Match 9.8%; Score 37; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 2.54e-85;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 GHLHSSILVPHGWRSRSHTHONHGHVNDSEWHP 217
Y 113 GHLHSSILVPHGWRSRSHTHONHGHVNDSEWHP 149

RESULT 6
ID 023824; PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEAMAYS (MAIZE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN-HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
differential expression to temperature.";
RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954; D1023306; -.
DR EMBL: D63952; D1023304; -.
DR PFM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;
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|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 9.5% | Score 36; | DB 10; | Length 443; |
| Best Local Similarity | 100.0%; | Pred. No. 3.81e-82; | | |
| Matches | 36; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

Dd 317 VTYLHHGHGHEDKLPYRGKEMSYLRGGITTLDRDYG 352
|||
Qy 251 VTYLHHGHGHEDKLPYRGKEMSYLRGGITTLDRDYG 286

| | | |
|--------|--------|--------------------------|
| RESULT | 7 | |
| ID | P93452 | PRELIMINARY; PRT; 438 AA |

DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
DE PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMEROPHYTA: TRACHEOPHYTA,
OC EUPHYLLOPHTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;
OC ASTERIDEAE: ARALIALES: APIACEAE: PETROSELINUM.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 97203190.
RX KIRSCH C., TAKAMURA-NIK M., REYNOLD S., HALLBROCK K., SOMSSICH I.E.,
RA "Rapid, transient, and highly localized induction of plastidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum.",
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
RL EMBL: U75745; ACAD. SCI. 94:2079-2084(1997).
DR PFAM: PF000487; FA desaturase; 1.
DR MENDEL: 97868; PETERC1208:1.
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 9.0%; | Score 34; | DB 10; | Length 438; |
| Best Local Similarity | 100.0%; | Pred. No. 8.01e-76; | | |
| Matches | 34; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

Db 180 LHSSILVPYHGKRIKSHRTTHQNHGAVENDESNRP 213
 |||
 Qy 116 LHSSILVPYHGKRIKSHRTTHQNHGAVENDESNRP 149

| | |
|--------------|--------|
| RESULT | 8 |
| ID | P94013 |
| PRELIMINARY; | PRT; |
| | 381 AA |

DT 01-MAY-1997 (TREMBLEL. 03. CREATED)
DT 01-MAY-1997 (TREMBLEL. 03. LAST SEQUENCE UPDATE)
DT 01-JUN-1999 (TREMBLEL. 03. LAST ANNOTATION UPDATE)
DE W-3 FATTY ACID DESATURASE.
DE ORYZA SATIVA (RICE).
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA
OC EUPHYLLIPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;
OC POACEAE: ORYZA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IR36, AND NIPPONBARE;
RA AKAGI H.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D78506; G177376; -;
DR EMBL: D78505; G1785856; -;
DR MENDEL, 9612; ORYZA.1208;1.
SQ SEQUENCE 381 AA: 43640 MW: 2BD4ED6E CRC32;

| | | | | |
|-----------------------|---------|---------------------|--------|--------------------------------|
| Query Match | 7.7%; | Score 29; | DB 10; | length 381; |
| Best Local Similarity | 100.0%; | Pred. No. 3.27e-60; | | |
| Matches | 29; | Conservative | 0; | Mismatches 0; Indels 0; Gaps 0 |

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Db      288  INNINHDIGTHVHHLFQPIRPHYLVEAT  316
        |||||
Oy      288  INNINHDIGTHVHHLFQPIRPHYLVEAT  316

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RESULT 9

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|----|--------|--------------|------|-----|-----|
| ID | 065792 | PRELIMINARY; | PRT; | 383 | AA. |
|----|--------|--------------|------|-----|-----|

AC 063/92/;
DT 01-AGG-1998 (TREMUREL. 07, CREATED)
DT 01-AGG-1998 (TREMUREL. 07, LAST SEQUENCE UPDATE)
DT 01-AGG-1998 (TREMUREL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
TARND3

OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.

RP SEQUENCE FROM N. A.
RC STRAIN-CV. CHIRIKU; TISSUE-LEAF, AND ROOT;
RA HORIGUCHI G., KAWAKAMI N., KUSUDI K.,
RL PLANT CELL PHYSIOL. 39:540-544(1998).
KODAMA H., IBA K.

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 7.7% | Score 29; | DB 10; | Length 383; |
| Best Local Similarity | 100.0%; | Pred. No. 3.27e-60; | | |
| Matches | 29; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

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Db      290  INNINHDIGTVIHNLFLRPQIRPHYLVEAT 318
          |||||
Qy      288  INNINHDIGTVIHNLFLRPQIRPHYLVEAT 316

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| | |
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| RESULT | 10 |
| ID | 064907 |
| | PRELIMINARY; |
| | PRT; |
| | 407 AA. |

DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE OMEGA-3 DESATURASE (FRAGMENT).
 GN PXH-15.
 OS EURKARIONTA X HORTORUM.
 OC PELLAGORIA; VIRIDIPILANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLLOPHYTES; GERANANTHOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE
 OC GERANIATALES; GERANIACEAE; PELARAGONIUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RP SCHULTZ D.J., MOMMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.,
 RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBD DATA BANKS.
 DR EMBL; AF020204; G3133389; -
 FT NON_TER 1
 SQ SEQUENCE 407 AA; 47166 MW; BC150974 CRC32;

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 7.4% | Score 28; | DB 10; | Length 407; |
| Best Local Similarity | 100.0%; | Pred. No. 3.96e-57; | | |
| Matches | 28; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

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Db      318 NNHHDIGTHVHNLFPQIRPHYHLEAT 343
      |||
QY      289 NNHHDIGTHVHNLFPQIRPHYHLEAT 316

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| | |
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| RESULT | 11 |
| ID | 023802 |
| | PRELIMINARY; |
| | PRT; |
| | 380 AA. |

DT 01-JAN-1998 (TREMABEL, 05, CREATED)
 DT 01-JAN-1998 (TREMABEL, 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMABEL, 08, LAST ANNOTATION UPDATE)
 DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
 GN TRITR7.
 OS TRITICUM AESTIVUM (WHEAT).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES
 EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; LILIOPSIDA; POALES;
 OC POACEAE; TRITICUM.

RN
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, CHIHOKU; TISSUE=LEAF;
 RA HORIGUCHI G., IWAKAWA H., KOYAMA H., KAWAKAMI N., NISHITURA M.,

RA IBA K.;
 RL PHYSIOL. PLANTARUM 96:275-283(1996).
 DR EMBL: D43688; D1008371; -.
 DR PFAM: PF00487; FA_desaturase; 1.
 FT NON_TER
 SQ SEQUENCE 380 AA; 42653 MW; 2123FF56 CRC32;

Query Match 6.3%; Score 24; DB 10; Length 380;
 Best Local Similarity 100.0%; Pred. No. 5.77e-45;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 GWRISHRTHONHGHVDESWHP 153
 126 GWRISHRTHONHGHVDESWHP 149

RESULT 12 PRELIMINARY; PRT; 359 AA.
 ID 055240
 AC 055240;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE DELTA 15 DESATURASE.
 GN DESB.
 OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
 OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95035996.
 RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
 RA MURATA N.,
 RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
 RT altering the degree of membrane-lipid unsaturation."
 RL PLANT MOL. BIOL. 26:249-263(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TABATA S.;
 RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAKOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions."
 RL DNA RES. 3:109-136(1996).
 DR EMBL: D13780; G600598; -.
 DR EMBL: D90913; G1653388; -.
 DR PFAM: PF00487; FA_desaturase; 1.
 SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;

Query Match 4.2%; Score 16; DB 2; Length 359;
 Best Local Similarity 100.0%; Pred. No. 8.34e-22;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPRHGRISHRTH 129
 120 ILVPRHGRISHRTH 135

RESULT 13 PRELIMINARY; PRT; 350 AA.
 ID 007872
 AC 007872;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE -OMEGA-3-DESATURASE.
 GN DESB.
 OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97260123.
 RA SAKAMOTO T., BRYANT D.A.;
 RT "Temperature-regulated mRNA accumulation and stabilization for fatty
 RT acid desaturase genes in the cyanobacterium Synechococcus sp. strain
 RT PCC 7002."
 RL MOL. MICROBIOL. 23:1281-1292(1997).
 DR EMBL: U36389; G2197199; -.
 DR PFAM: PF00487; FA_desaturase; 1.
 SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;

Query Match 2.9%; Score 11; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 8.89e-09;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 74 AOGTFFWALFY 84
 82 AOGTFFWALFY 92

RESULT 14 PRELIMINARY; PRT; 193 AA.
 ID 074645
 AC 074645;
 DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE FATTY ACID DESATURASE (FRAGMENT).
 OS GIBBERELLA ZEAE.
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
 OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-F15;
 RX MEDLINE: 98433864.
 RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
 RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
 RT Analysis of the region around Trl01 and characterization of its
 RT homologue from Fusarium sporotrichoides."
 RL FEBS LETT. 435:163-168(1998).
 DR EMBL: AB014492; D1034743; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 2.1%; Score 8; DB 3; Length 193;
 Best Local Similarity 100.0%; Pred. No. 4.64e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 HVHHLFP 193
 298 HVHHLFP 305

RESULT 15 PRELIMINARY; PRT; 598 AA.
 ID 044316
 AC 044316;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE MALTOLOGOSYL TREHALOSE TREHALOHYDROLASE.
 GN TREZ.
 OS ARTHROBACTER SP.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIAE;
 OC ACTINOMYCETALES; MICROCOCCINAE; MICROCOCCACEAE; ARTHROBACTER.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Q36;
 RX MEDLINE: 96195835.
 RA MARUTA K., HATORI K., NAKADA T., KUBOTA M., SUGIMOTO T., KURIMOTO M.;
 RT "Cloning and sequencing of trehalose biosynthesis genes from
 RT Arthrobacter sp. Q36.";

```

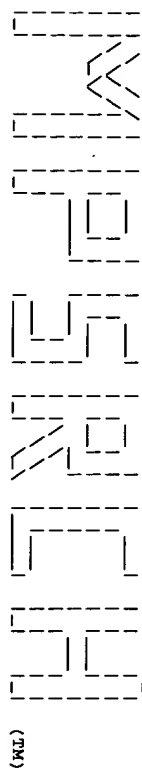
RL  BIOCHIM. BIOPHYS. ACTA 1289:10-13(1996).
DR  EMBL; D63343; D1010313; -.
DR  PFAA; PF00128; alpha-amylase; 1.
KW  HYDROLASE.
SQ  SEQUENCE 598 AA; 65832 MW; 22719107 CRC32;

Query Match      2.18; Score 8; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.64e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      8 EAAKPYLG 15
      |||||
QY      317 EAAKPYLG 324
  
```

Search completed: Sat Aug 21 12:26:12 1999
 Job time : 98 secs.

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Msearch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:18:17 1999; Maspar time 15.09 Seconds
532.719 Million cell updates/sec

Tabular output not generated.

Title: >US-09-219-935-7
Description: (1-378) from US0921935.pep
Perfect Score: 378
Sequence: 1 LTVDSSTSPTEEPKTRF.....DVVYVYADPNLXGKTKYAE 378

Scoring table: TABLE uniprottable
Gap 60

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.891; Variance 0.684; scale 4.229

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------------------|
| 1 | 378 | 100.0 | 378 | 7 | R37591 | Sequence of microsoma |
| 2 | 378 | 100.0 | 404 | 7 | R37594 | Sequence of plastid d |
| 3 | 103 | 27.2 | 446 | 11 | R60499 | Linoleic-acid-desatur |
| 4 | 103 | 27.2 | 446 | 7 | R37593 | Sequence of a plastid |
| 5 | 43 | 11.4 | 435 | 11 | R60500 | Linoleic-acid-desatur |
| 6 | 36 | 9.5 | 447 | 24 | W13381 | Sesame omega-3 alpha |
| 7 | 36 | 9.5 | 453 | 7 | R37596 | Sequence of soybean p |
| 8 | 30 | 7.9 | 156 | 7 | R37598 | Sequence of a plastid |
| 9 | 28 | 7.4 | 383 | 11 | R60498 | Linoleic-acid-desatur |
| 10 | 28 | 7.4 | 386 | 7 | R37592 | Sequence of delta-15 |
| 11 | 27 | 7.1 | 380 | 7 | R37595 | Sequence of microsoma |
| 12 | 27 | 7.1 | 125 | 7 | R37597 | Sequence of an intern |
| 13 | 9 | 2.4 | 387 | 10 | R37600 | Sequence of corn mltc |
| 14 | 8 | 2.1 | 20 | 14 | R80294 | Trehalose releasing e |
| 15 | 8 | 2.1 | 597 | 14 | R80290 | Trehalose releasing e |
| 16 | 8 | 2.1 | 598 | 14 | R77471 | Trehalose releasing e |

| Result ID | Score | Query Match | Length | ID | Description | Pred. No. |
|-----------|-------|-------------|--------|----|-------------|---------------------------|
| 17 | 7 | 1.9 | 18 | 17 | R88585 | Spider venom calcium |
| 18 | 7 | 1.9 | 18 | 2 | R07633 | N-terminal of Fractio |
| 19 | 7 | 1.9 | 18 | 8 | R38424 | A. aperta venom fractio |
| 20 | 7 | 1.9 | 236 | 26 | W37715 | C. glutamicum lys E p |
| 21 | 7 | 1.9 | 289 | 19 | W01128 | Coat protein (short v |
| 22 | 7 | 1.9 | 367 | 19 | R98899 | Coat protein (long ve |
| 23 | 7 | 1.9 | 367 | 34 | W61492 | Human fetuin glycopro |
| 24 | 7 | 1.9 | 663 | 4 | R24101 | Marek's disease virus |
| 25 | 6 | 1.6 | 202 | 39 | W67822 | Human secreted protei |
| 26 | 6 | 1.6 | 203 | 39 | W67898 | Human secreted protei |
| 27 | 6 | 1.6 | 239 | 36 | W80690 | S. pneumoniae protein |
| 28 | 6 | 1.6 | 248 | 5 | R25573 | Mature alpha-TTichosa |
| 29 | 6 | 1.6 | 267 | 23 | W21703 | H. pylori secreted or |
| 30 | 6 | 1.6 | 373 | 22 | W20833 | Human growth-related |
| 31 | 6 | 1.6 | 424 | 39 | W86150 | B. subtilis Yade rela |
| 32 | 6 | 1.6 | 438 | 39 | W95500 | Human protein-couple |
| 33 | 6 | 1.6 | 493 | 39 | W84068 | Human mitochondriin Fzo h |
| 34 | 6 | 1.6 | 519 | 39 | W89782 | Staphylococcus aureus |
| 35 | 6 | 1.6 | 539 | 37 | W76281 | Coprinus cinereus lac |
| 36 | 6 | 1.6 | 549 | 38 | W70898 | Acetyl-coenzyme A tra |
| 37 | 6 | 1.6 | 707 | 38 | W83395 | Rabbit protein-couple |
| 38 | 6 | 1.6 | 708 | 38 | W83394 | Human protein-couple |
| 39 | 6 | 1.6 | 844 | 19 | R86952 | E. coli PBP 1B transg |
| 40 | 6 | 1.6 | 1012 | 39 | W95395 | IBDV VP2-VP3-VP4 poly |
| 41 | 6 | 1.6 | 1978 | 35 | W69361 | Tetradotoxin-sensitiv |
| 42 | 6 | 1.6 | 1988 | 35 | W69362 | Tetradotoxin-sensitiv |
| 43 | 6 | 1.6 | 2100 | 39 | W89579 | Calcium permeable vol |
| 44 | 6 | 1.6 | 2104 | 39 | W89578 | Calcium permeable vol |
| 45 | 6 | 1.6 | 2105 | 39 | W89577 | Calcium permeable vol |

ALIGNMENTS

RESULT 1
ID R37591 standard; Protein; 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition, modification, fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF3-f2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU POINT DE NEMOURS & CO E. I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR NPI: 93-197063/24.
DR N-PDB: 043205.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 136-138; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing valid-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA:
Query Match 100.0%; Score 378; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ltvdsassprleeeptqrfpbgappfnadiraipkhwvknpmkmsyvvrelaiiv 60
   |||||
QY 1 LTVSSSSPPIEEBPKTORFDPGAPPPNLAIDRAIPKHWKNPMKMSYVRELAIIV 60

Db 61 falaagaaylwnwlvwplwylwlaaggtumfvalfvlgchdcghsfsndprlnsvvghllhssi 120
   |||||
QY 61 FALAAGAAYLWNWLVWPLWYLAOGTFMVALFVLGCHDCGHGSFSDNDRPLNSVVGHLHSSI 120

Db 121 lvpvghwvishrthqnhghvendeswhpmseklyksldkptcrtffrtflplwmlayfpyl 180
   |||||
QY 121 LVPVGHWMISHRTHQNHGHVENDESWHPMSEKITYKSLDKPTRFRFTPLPLWMLAYFPYL 180

Db 181 warspgkgsghyhpdsdlflpkerndvltstacwtamaavlvcnlfmymgmmlklyvip 240
   |||||
QY 181 WARSFGKGSYHPDSDFLPKERNVDLTSTACWTAMAAVLLVCNLFYMGPMQMLKLYVIP 240

Db 241 ywlnvmwldfvtlylhhghedklpwyrgekwsylrgglttldrdyglinnihhdigthvi 300
   |||||
QY 241 YWINVMWLDFTVYLHHGHEDKLPWYRGKEMSYLRGGLTTLDROYGLINNIIHHDIGTHVI 300

Db 301 hhlfrqjphylhveateaakpvlqkyrepdksgprlhlhlgilaksikedhfvdsedgv 360
   |||||
QY 301 HHLFPQJPHYHLVEATEAKPVLGKYREPKSGPLRHLHGLIAKSIKEDHFVDSGDV 360

Db 361 vyyeadpnllygelkvtiae 378
   |||||
QY 361 VYEADPNLYGEIKVTAE 378

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RESULT 2
ID R37594 standard; Protein; 404 AA.
AC R37594;
DE 01-OCT-1993 (first entry)
KW Sequence of plastid delta-15 glycerolipid desaturase.
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF-2.
PN W09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43206.
PT Isolated nucleic acid fragment, for plant lipid composn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. The cDNA inserts
CC was deposited at ATCC No. 68854. PBNSF3-3 (Q43206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 404 AA;

```

```

Query Match 100.0%; Score 378; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.0e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Db 27 ltvdsassprleeeptqrfpbgappfnadiraipkhwvknpmkmsyvvrelaiiv 86
   |||||
QY 1 LTVSSSSPPIEEBPKTORFDPGAPPPNLAIDRAIPKHWKNPMKMSYVRELAIIV 60

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Db 87 falaagaaylwnwlvwplwylwlaaggtumfvalfvlgchdcghsfsndprlnsvvghllhssi 146
   |||||
QY 61 FALAAGAAYLWNWLVWPLWYLAOGTFMVALFVLGCHDCGHGSFSDNDRPLNSVVGHLHSSI 120

Db 147 lvpvghwvishrthqnhghvendeswhpmseklyksldkptcrtffrtflplwmlayfpyl 206
   |||||
QY 121 LVPVGHWMISHRTHQNHGHVENDESWHPMSEKITYKSLDKPTRFRFTPLPLWMLAYFPYL 180

Db 207 warspgkgsghyhpdsdlflpkerndvltstacwtamaavlvcnlfmymgmmlklyvip 266
   |||||
QY 181 WARSFGKGSYHPDSDFLPKERNVDLTSTACWTAMAAVLLVCNLFYMGPMQMLKLYVIP 240

Db 267 ywlnvmwldfvtlylhhghedklpwyrgekwsylrgglttldrdyglinnihhdigthvi 326
   |||||
QY 241 YWINVMWLDFTVYLHHGHEDKLPWYRGKEMSYLRGGLTTLDROYGLINNIIHHDIGTHVI 300

Db 327 hhlfrqjphylhveateaakpvlqkyrepdksgprlhlhlgilaksikedhfvdsedgv 386
   |||||
QY 301 HHLFPQJPHYHLVEATEAKPVLGKYREPKSGPLRHLHGLIAKSIKEDHFVDSGDV 360

Db 387 vyyeadpnllygelkvtiae 404
   |||||
QY 361 VYEADPNLYGEIKVTAE 378

```

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RESULT 3
ID R60499 standard; Protein; 446 AA.
AC R60499;
DE 28-MAR-1995 (first entry)
KW Lipoic-acid-desaturase fadd; transgenic plant; crop improvement;
KW Lipoic-acid-desaturase; fadd; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS.) MONSANTO CO.
PA (UNMS.) UNIV MICHIGAN STATE.
PI Alondel VJA, Gibson SJ, Kishore GM, Ruff TG, Somerville CR;
PI WPI: 94-279758/34.
DR N-PSDB: Q71210.
PT Genetically transformed plants with altered lipoic acid
PT content - contg recombinant, double-stranded DNA encoding
PT lipoic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 75-77; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of lipoic-
CC acid-desaturase fadd of Arabidopsis are provided.
SQ Sequence 446 AA;

```

```

Query Match 27.2%; Score 103; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.3e-163;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 307 lpyvlnvmwldfvtlylhhghedklpwyrgekwsylrgglttldrdyglinnihhdigthvi 366
   |||||
QY 239 IPYVINVMWLDFTVYLHHGHEDKLPWYRGKEMSYLRGGLTTLDROYGLINNIIHHDIGTH 298

Db 367 vlhhlfrqjphylhveateaakpvlqkyrepdksgprlhlhlgilaksikedhfvdsedgv 409
   |||||
QY 299 VHLHLPQJPHYHLVEATEAKPVLGKYREPKSGPLRHLHGLIAKSIKEDHFVDSGDV 341

```

PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43204.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 132-134; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. In contrast to the
 CC constitutive expression of the gene encoding (R37592), the mRNA
 CC corresponding to Q43204 is abundant in green tissues, rare in roots
 CC and leaves, and is about three-fold more abundant in leaf than that
 CC of Q43202. R37592 and R37593 show and overall homology of approx.
 CC 80%.

Sequence 446 AA;

Query Match 27.2%; Score 103; DB 7; Length 446;
 Best Local Similarity 100.0%; Pred. No. 7.36e-163;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 lgyvlnvmldfvtvlyhhghedklypryrgkewsyrlrglttdrtyglinnhhdtgch 366
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 239 lryvlnvmldfvtvlyhhghedklypryrgkewsyrlrglttdrtyglinnhhdtgch 298
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 367 vlhhlfpqlyphylhveateakpvlgyrgepdksqplrlhll 409
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 299 vlnhlfpoiprhyhlvateakpvlgyrgepdksqplrlhll 341
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 5
 ID R60500 standard; Protein: 435 AA.
 AC R60500;

DT 28-MAR-1995 (first entry)
 DE linoleic acid-desaturase fadE.
 KW linoleic acid-desaturase; fadE; transgenic plant; crop improvement;
 KM linoleic acid.
 OS Arabidopsis.
 PN MO9418337-A.
 PD 18-AUG-1994.
 PF 04-FEB-1994; U01321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Aronold VZA, Gibson ST, Kishore GM, Ruif TG, Somerville CR;
 DR WPI: 94-279768/34.
 DR N-PSDB: Q71211.
 PT Genetically transformed plants with altered linoleic acid
 PT content - conty recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence
 PS Disclosure; Page 79-81; 144pp; English.
 CC The cDNA sequence and deduced amino acid sequence of linoleic-
 CC acid-desaturase fadE of Arabidopsis are provided.

Query Match 11.4%; Score 43; DB 11; Length 435;
 Best Local Similarity 100.0%; Pred. No. 6.52e-57;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 lnnlhhdigtvlyhhlfpqlyphylhveateakpvlgyrgepd 391
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 288 lnnlhhdigtvlyhhlfpqlyphylhveateakpvlgyrgepd 330
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 6
 ID W13381 standard; Protein: 447 AA.
 AC W13381;

DT 02-DEC-1997 (first entry)
 DE Sesame omega-3 aliphatic acid desaturase.
 KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
 KM linoleic acid; recombinant production.
 OS Sesamum indicum.
 PN J09065882-A.
 PD 11-MAR-1997.
 PR 01-SEP-1995; 225145.
 PR 01-SEP-1995; JP-225145.
 PA (TOYA-) TOYAMA KEN.
 DR WPI: 97-220417/20.
 DR N-PSDB: T62066.
 PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
 PT engineering to modify fats and oils in agricultural products
 PS Claim 6; Page 4; 10pp; Japanese.
 CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
 CC sequence can be used in genetic engineering to modify fats and oils in
 CC agricultural products. The gene or enzyme can be introduced into a plant
 CC to modify the aliphatic acid composition in its oils and fats, to give
 CC oils and fats with a high content of linoleic acid. Antisense DNA can
 CC be introduced into a plant to inhibit the expression of the gene, so
 CC that oils and fats with little or no linoleic acid are produced. The
 CC gene can also be expressed in microorganisms for recombinant production
 CC the enzyme.

Sequence 447 AA;

Query Match 9.5%; Score 36; DB 24; Length 447;
 Best Local Similarity 100.0%; Pred. No. 6.44e-45;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 323 vtyllhghedklypryrgkewsyrlrglttdrtyg 358
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 251 vtyllhghedklypryrgkewsyrlrglttdrtyg 286
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 7
 ID R37596 standard; Protein: 453 AA.
 AC R37596;

DT 01-OCT-1993 (first entry)
 DE Sequence of soybean plastid delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Glycine max, clone pSFD-118bp.
 PN WO9311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43208.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure; Page 148-150; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the pCF3
 CC insert was also used. The identity of the expression product of pCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15

CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC deposited under ATCC 68874. Soybean microsomal delta-15
CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC encoding related desaturases from soybean. The insert of
CC pSPD-11bwp contained a stretch of 1675 nucleotides which contained
CC an open-reading frame encoding a polypeptide (R37596) of about
CC 80% identity with, and colinear with, the Arabidopsis plastid
CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC to 382 encode the putative plastid transit peptide, colinear with
CC and sharing some homology with the transit peptide described for
CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ Sequence 453 AA;

Query Match 9.5%; Score 36; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 6.44e-45;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 vtylhhghedk1pwyrgkwsy1rgglttdtdyg 362
|
OY 251 VTYLHHGHEDKLPWYRGKWSYLRGGLTTLDRDYG 286

RESULT 8
ID R37598 standard; Protein; 156 AA.
AC R37598;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pfxdx-2 and pfxpc7.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS; 93-197063/24.
DR WPI; 93-197063/24.
N-PSDB; Q43210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q4324. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pfxdx-2 and
CC pfxpc7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 7.9%; Score 30; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.83e-35;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 aggtmfwalfv1ghdcgfsfndprlnsv 124
|
OY 82 AGGTMFWALFVLGHDCGFSFNDPRLNSV 111

RESULT 9
ID R60498 standard; Protein; 383 AA.
AC R60498;
DT 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase; fad3.
KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
KW transgenic plant; crop improvement; yeast artificial chromosome;

KW YAC; linoleic acid.
OS Brassica napus.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Aronold VM, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI; 94-279758/34.
N-PSDB; Q71203.
PT Genetically transformed plants with altered linoleic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 69-71; 144pp; English.
CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
CC isolated from a YAC library using RFLP 220 and ASA2 markers as
CC probes. Isolated DNA was amplified using the primers given in
CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
CC identified in YAC EW7D11.
SQ Sequence 383 AA;

Query Match 7.4%; Score 28; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.93e-31;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 llvpygwrlshrtbhqnhvendesw 150
|
OY 120 LLVPGWRLSHRTHQHNGHVENDESW 147

RESULT 10
ID R37592 standard; Protein; 386 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pcf3.
PN M09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS; 93-197063/24.
DR WPI; 93-197063/24.
N-PSDB; Q43202.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 127-129; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224.
SQ Sequence 386 AA;

Query Match 7.4%; Score 28; DB 7; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.93e-31;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 llvpygwrlshrtbhqnhvendesw 153
|
OY 120 LLVPGWRLSHRTHQHNGHVENDESW 147

RESULT 11
ID R37595 standard; Protein: 380 AA.
AC R37595;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase,
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pXf1.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992; U10284.
PI 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043207.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 144-146; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC deposited under ATCC 68874.
SQ Sequence 380 AA;

Query Match 7.1%; Score 27; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 8.83e-30;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 nhhdtghvhhlfqqlphylveat 321
|||
QY 290 NHHDTGHVHHLFQQLPHYLVEAT 316

RESULT 12
ID R37597 standard; Protein: 126 AA.
AC R37597;
DT 01-OCT-1993 (first entry)
DE Sequence of an internal region of a corn seed delta-15
DE desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Zea mays; clone pPCR20.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992; U10284.
PI 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043209.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 152-153; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43209 is the
CC complete nucleotide sequence of a 396 bp polymerase chain reaction
CC product derived from corn seed mRNA that is found in the insert of
CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to
CC the amplification primers described in Q43211 and Q43212
CC respectively. Nucleotides 31 to 363 encode a region that is 61.9%
CC identical to the region between amino acids 137 and 249 of R37591.
SQ Sequence 126 AA;

Query Match 2.4%; Score 9; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 5.61e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 vtylhhgh 126
|||||
QY 251 VTYLHHGH 259

RESULT 13
ID R53700 standard; Protein: 387 AA.
AC R53700;
DT 09-NOV-1994 (first entry)
DE Sequence of corn microsomal delta-12 desaturase deduced from the
DE cDNA in plasmid pFad2 1.
KW Fatty acid; desaturase; lipid; unsaturated; transgenic plant.
OS Zea mays.
PN W09411516-A.
PD 26-MAY-1994.
PR 15-OCT-1993; U09987.
PI 17-NOV-1992; US-977339.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Lightner JE, Okuley JJ;
DR WPI: 94-183515/22.
DR N-PSDB: Q66071.
PT Genes for fatty acid desaturase enzymes - permit alteration of
PT lipid composition
PS Claim 13; Page 124-126; 147pp; English.
CC Corn microsomal delta-12 desaturase cDNA was isolated using a PCR
CC approach. A cDNA library was made to poly A+ mRNA from developing
CC corn embryos. This library was used as template for PCR using sets
CC of degenerate oligos NS3 (Q66075) and RB5A/B (Q66077, Q66078) as
CC sense and antisense primers, respectively. NS3 and RB5A/B corresp.
CC to stretches of AAs 101-109 and 318-326, respectively, of R53697,
CC which are conserved in most microsomal delta-12 desaturases. A PCR
CC product of 720bp was purified and used as a probe for screening the
CC corn cDNA library. A plaque was purified and found to encode
CC microsomal delta-12 desaturase truncated at the 3' end. This cDNA
CC was used to probe the corn cDNA library again. The clone contg.
CC (Q66071). An isolated nucleic acid fragment
CC wherein the nucleic acid identity is 90% or greater to
CC Q66071 is claimed. A method to isolate nucleic acid fragments
CC encoding fatty acid desaturases and related enzymes is claimed
CC which comprises: comparing AA sequences in R53697-R53702 and other
CC fatty acid desaturase sequences; identifying conserved sequences of
CC 4 or more AAs; designing degenerate oligos based on the conserved
CC sequences; and using the oligos to isolate sequences encoding fatty
CC acid desaturases and desaturase-related enzymes.
SQ Sequence 387 AA;

Query Match 2.4%; Score 9; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.61e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 92 wplywiag 100
|||||
QY 76 WPLYWIAG 84

RESULT 14
ID R80294 standard; Protein: 20 AA.

AC R80294: (first entry)
 DE 19-JAN-1996 (first entry)
 DE trehalose releasing enzyme N-terminal fragment.
 KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
 KW alpha-maltotriose; alpha-maltotetraose; maltopentaosyltrehalose;
 KW maltopentaosyltrehalose; sweetener; taste-improving agent;
 KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
 KW pharmaceuticals.
 OS Archaeobacter sp. Q36.
 PN EP-671470-A2.
 PD 13-SEP-1995.
 PF 07-MAR-1995: 301474.
 PR 07-MAR-1994: JP-059840.
 PR 07-MAR-1994: JP-059834.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
 DR WPI: 95-312772/41.
 PT DNA encoding a trehalose releasing enzyme - which releases trehalose
 from a non-reducing saccharide having a trehalose structure as an
 end unit.
 PS Example 4; Page 25; 45pp; English.
 CC The trehalose releasing enzyme can be used for the preparation of
 trehalose with high yields and efficiency from non-reducing
 saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
 alpha-maltotriose, alpha-maltotetraose, alpha-maltopentaosyltrehalose and
 maltopentaosyltrehalose. The trehalose can be used as a sweetener,
 taste-improving agent, quality-improving agent, stabiliser, filler,
 excipient or adjuvant in food products cosmetics and pharmaceuticals.
 CC This is the N-terminal sequence of the enzyme.
 SQ Sequence 20 AA:

Query Match 2.1%; Score 8; DB 14; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.08e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 7 eaakpvlq 14
 |||||
 QY 317 EAAKPVLG 324

RESULT 15
 ID R80290 standard; Protein; 597 AA.
 AC R80290:
 DE 19-JAN-1996 (first entry)
 DE trehalose releasing enzyme.
 KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
 KW alpha-maltotriose; alpha-maltotetraose; maltopentaosyltrehalose;
 KW maltopentaosyltrehalose; sweetener; taste-improving agent;
 KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
 KW pharmaceuticals.
 OS Archaeobacter sp. Q36.
 PN EP-671470-A2.
 PD 13-SEP-1995.
 PF 07-MAR-1995: 301474.
 PR 07-MAR-1994: JP-059840.
 PR 07-MAR-1994: JP-059834.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
 DR WPI: 95-312772/41.
 DR N-PSDB: 098670.
 PT DNA encoding a trehalose releasing enzyme - which releases trehalose
 from a non-reducing saccharide having a trehalose structure as an
 end unit.
 PS Claim 3; Page 24-25; 45pp; English.
 CC This enzyme can be used for the preparation of trehalose with high
 yields and efficiency from non-reducing saccharides such as
 alpha-glucosyltrehalose, alpha-maltosyltrehalose,
 alpha-maltotriose, alpha-maltotetraose, alpha-maltopentaosyltrehalose and
 maltopentaosyltrehalose. The trehalose can be used as a sweetener,
 taste-improving agent, quality-improving agent, stabiliser, filler,
 excipient or adjuvant in food products cosmetics and pharmaceuticals.
 SQ Sequence 597 AA:

Query Match 2.1%; Score 8; DB 14; Length 597;
 Best Local Similarity 100.0%; Pred. No. 1.08e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 7 eaakpvlq 14
 |||||
 QY 317 EAAKPVLG 324

Search completed: Sat Aug 21 12:22:23 1999
 Job time : 246 secs.

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Msarch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:26:29 1999; Maspar time 4.93 Seconds

Tabular output not generated. 777.764 Million cell updates/sec

Title: >US09-219-935-7

Description: (1-378) from US09219935.pep

Sequence: 1 LTVDSSTPPIEEPKTORF.....DVYYEADPNLGEIKVTAE 378

Scoring table: TABLE uniprottable

Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 2-issued
#5A_COMB 2:5B_COMB 3:PCRT9_COMB 4:backfiles1

Statistics: Mean 2.741; Variance 0.681; scale 4.025

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 378 | 100.0 | 378 | 3 | PCT-US92-1 Sequence 7, Applicatio | 0.00e+00 |
| 2 | 378 | 100.0 | 404 | 3 | PCT-US92-1 Sequence 9, Applicatio | 0.00e+00 |
| 3 | 103 | 27.2 | 446 | 3 | PCT-US94-0 Sequence 10, Applicati | 4.67e-156 |
| 4 | 103 | 27.2 | 446 | 3 | PCT-US92-1 Sequence 5, Applicatio | 4.67e-156 |
| 5 | 43 | 11.4 | 435 | 3 | PCT-US94-0 Sequence 12, Applicati | 5.66e-55 |
| 6 | 36 | 9.5 | 453 | 3 | PCT-US92-1 Sequence 13, Applicati | 1.66e-43 |
| 7 | 31 | 8.2 | 156 | 3 | PCT-US92-1 Sequence 17, Applicati | 2.06e-35 |
| 8 | 28 | 7.4 | 383 | 3 | PCT-US94-0 Sequence 2, Applicatio | 1.31e-30 |
| 9 | 28 | 7.4 | 386 | 3 | PCT-US92-1 Sequence 2, Applicatio | 1.31e-30 |
| 10 | 27 | 7.1 | 380 | 3 | PCT-US92-1 Sequence 11, Applicati | 5.11e-29 |
| 11 | 25 | 6.6 | 37 | 2 | US-08-320- Sequence 6, Applicatio | 7.46e-26 |
| 12 | 25 | 6.6 | 37 | 2 | US-08-320- Sequence 22, Applicati | 7.46e-26 |
| 13 | 25 | 6.6 | 37 | 1 | US-08-314- Sequence 6, Applicatio | 7.46e-26 |
| 14 | 25 | 6.6 | 37 | 1 | US-08-314- Sequence 22, Applicati | 7.46e-26 |
| 15 | 22 | 5.8 | 37 | 1 | US-08-314- Sequence 16, Applicati | 3.68e-21 |
| 16 | 22 | 5.8 | 37 | 1 | US-08-314- Sequence 12, Applicati | 3.68e-21 |
| 17 | 22 | 5.8 | 37 | 2 | US-08-320- Sequence 16, Applicati | 3.68e-21 |
| 18 | 22 | 5.8 | 37 | 2 | US-08-320- Sequence 12, Applicati | 3.68e-21 |
| 19 | 18 | 4.8 | 40 | 2 | US-08-320- Sequence 10, Applicati | 4.96e-15 |
| 20 | 18 | 4.8 | 40 | 2 | US-08-320- Sequence 18, Applicati | 4.96e-15 |
| 21 | 18 | 4.8 | 40 | 1 | US-08-314- Sequence 10, Applicati | 4.96e-15 |
| 22 | 18 | 4.8 | 40 | 1 | US-08-314- Sequence 18, Applicati | 4.96e-15 |
| 23 | 12 | 3.2 | 37 | 1 | US-08-314- Sequence 26, Applicati | 2.82e-06 |

ALIGNMENTS

| RESULT ID | 1 | STANDARD | PRT | 378 AA. |
|-----------|---|----------|-----|---------|
| XX | PCT-US92-10284-7 | | | |
| XX | xxxxxx | | | |
| XX | Sequence 7, Application PC/TUS9210284 | | | |
| DE | Sequence 7, Application PC/TUS9210284 | | | |
| CC | GENERAL INFORMATION: | | | |
| CC | APPLICANT: Browne, John, Kinney, Anthony J., | | | |
| CC | APPLICANT: Pierce, John, Wierzbicki, Anna M., | | | |
| CC | APPLICANT: Yadav, Narendra S., Perez-Grau, Luis | | | |
| CC | TITLE OF INVENTION: Fatty Acid Desaturase Genes | | | |
| CC | NUMBER OF SEQUENCES: 32 | | | |
| CC | CORRESPONDENCE ADDRESS: | | | |
| CC | ADDRESSEE: E. I. du Pont de Nemours and Company | | | |
| CC | STREET: 1007 Market Street | | | |
| CC | CITY: Wilmington | | | |
| CC | STATE: Delaware | | | |
| CC | COUNTRY: U.S.A. | | | |
| CC | ZIP: 19898 | | | |
| CC | COMPUTER READABLE FORM: | | | |
| CC | MEDIUM TYPE: Floppy disk | | | |
| CC | COMPUTER: Macintosh | | | |
| CC | OPERATING SYSTEM: Macintosh System, 6.0 | | | |
| CC | SOFTWARE: Microsoft Word, 4.0 | | | |
| CC | CURRENT APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: PCT/US92/10284 | | | |
| CC | FILING DATE: 19921203 | | | |
| CC | CLASSIFICATION: 435 | | | |
| CC | PRIOR APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: 07/804,259 | | | |
| CC | FILING DATE: 4 DECEMBER 1991 | | | |
| CC | ATTORNEY/AGENT INFORMATION: | | | |
| CC | NAME: Floyd, Linda A. | | | |
| CC | REGISTRATION NUMBER: 33,692 | | | |
| CC | REFERENCE/DOCKET NUMBER: BB-1036-A | | | |
| CC | TELECOMMUNICATION INFORMATION: | | | |
| CC | TELEPHONE: (302) 992-4929 | | | |
| CC | TELEFAX: (302) 892-7949 | | | |
| CC | TELEX: 835420 | | | |
| CC | INFORMATION FOR SEQ ID NO: 7: | | | |
| CC | SEQUENCE CHARACTERISTICS: | | | |
| CC | LENGTH: 378 amino acids | | | |

| | | |
|-------------|---|--|
| | TYPE: | AMINO ACID |
| CC | TOPOLOGY: | linear |
| CC | MOLECULE TYPE: | protein |
| SQ | SEQUENCE | 378 AA; 43528 MW; 793455 CN; |
| | Query Match | 100.0%; Score 378; DB 3; Length 378; |
| | Best Local Similarity | 100.0%; Pred. No. 0.00e+00; |
| | Matches 378; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| D | 1 | LTVSSSPPIIEEPKTORFDGAPPEPNLADIRAAIPKHCWKNPKMSYVRELAIY 60 |
| O | 1 | LTVSSSSPPIIEEPKTRGRFDPGARPPENLADIHAALPKHCWKVNPKMSYVRELAIY 60 |
| D | 61 | FALAAGAYLNWLWPPLYTAOGTMTVALFYLGCHDGHGSNDPLNSVYGHLHSSI 120 |
| O | 61 | FALAAGAYLNNMWLPWPLYTAOGTMTVALFLVGLGDGHGSFSDPRLNSVYGHLLHSSI 120 |
| D | 121 | LVPHGWSISRTHONHNGHVENEDESMHPSEKIYKSLDKPTREFRFTPLVMATPYFL 180 |
| O | 121 | LVPHTGWISIRTHONHNGHVENEDESMHPSEKIYKSLDKPTREFRFTPLVMATPYFL 180 |
| D | 181 | WARSGKGKSHYHRPDSDFLEPKRENDVLTSTACTATAVAVLVCNLFMGSPQMILKVIP 240 |
| O | 181 | WARSGKKGSHYHRPDSDFLEPKRENDVLTSTACTATAVAVLVCNLFMGSPQMILKVIP 240 |
| D | 241 | TWINVMILDEVTTYHHGHEDKLFMYRGKEKSYLRGGLTTLDROYGLINNHHDIQTHVI 300 |
| O | 241 | TWINVMILDEVTTYHHGHEDKLFMYRGKEKSYLRGGLTTLDROYGLINNHHDIQTHVI 300 |
| D | 301 | HHLPRQIHYHLVETEAAPVKLYKYREPDKSGPLPHLIGLIAKSIEDHFVSDEGDV 360 |
| O | 301 | HHLPRQIHYHLVETEAAPVKLYKYREPDKSGPLPHLIGLIAKSIEDHFVSDEGDV 360 |
| D | 361 | VYEADPNLYGEIKVTAE 378 |
| O | 361 | VYEADPNLYGEIKVTAE 378 |
| RESULT | 2 | |
| ID | PCT-US92-10284-9 | STANDARD: PRT: 404 AA. |
| AC | xxxxxx | |
| DT | | |
| XX | | |
| XX | | |
| Sequence 9, | Application PC/TUS9210284 | |
| XX | | |
| CC | Sequence 9, Application PC/TUS9210284 | |
| CC | GENERAL INFORMATION: | |
| CC | APPLICANT: Browne, John, Kinney, Anthony J., | |
| CC | APPLICANT: Pierce, John, Wierzbicki, Anna M., | |
| CC | APPLICANT: Yadav, Narendra S., Perez-Grau, Luis | |
| CC | TITLE OF INVENTION: Fatty Acid Desaturase Genes | |
| CC | TITLE OF INVENTION: from Plants | |
| CC | NUMBER OF SEQUENCES: 32 | |
| CC | CORRESPONDENCE ADDRESS: | |
| CC | ADDRESSEE: E. I. du Pont de Nemours and Company | |
| CC | STREET: 1007 Market Street | |
| CC | City: Wilmington | |
| CC | STATE: Delaware | |
| CC | COUNTRY: U.S.A. | |
| CC | ZIP: 19898 | |
| CC | COMPUTER READABLE FORM: | |
| CC | MEDIUM TYPE: Floppy disk | |
| CC | COMPUTER: Macintosh | |
| CC | OPERATING SYSTEM: Macintosh System, 6.0 | |
| CC | SOFTWARE: Microsoft Word, 4.0 | |
| CC | CURRENT APPLICATION DATA: | |
| CC | APPLICATION NUMBER: PCT/US92/10284 | |
| CC | FILING DATE: 19921203 | |
| CC | CLASSIFICATION: 435 | |
| CC | PRIOR APPLICATION DATA: | |
| CC | APPLICATION NUMBER: 07/804,259 | |

| | | |
|---------------------------|---|---|
| CC | FILING DATE: | 4 DECEMBER 1991 |
| CC | ATTORNEY/AGENT INFORMATION: | |
| CC | NAME: | FLOYD, Linda A. |
| CC | REGISTRATION NUMBER: | 33,692 |
| CC | REFERENCE/DOCKET NUMBER: | BB-1036-A |
| CC | TELECOMMUNICATION INFORMATION: | |
| CC | TELEPHONE: | (302) 992-4929 |
| CC | TELEFAX: | (302) 892-7949 |
| CC | TELEX: | 835420 |
| CC | INFORMATION FOR SEQ ID NO: | 9: |
| CC | SEQUENCE CHARACTERISTICS: | |
| CC | LENGTH: | 404 amino acids |
| CC | TYPE: | AMINO ACID |
| CC | TOPOLOGY: | Linear |
| CC | MOLECULE TYPE: | protein |
| CC | SEQUENCE | 404 AA; 46617 MW; 906055 CN; |
| SQ | | |
| | Query Match | 100.0%; Score 378; DB 3; Length 404; |
| | Best Local Similarity | 100.0%; Fred. No. 0.00e+00; |
| | Matches | 378; Conservative 0; Mismatches 0; Indels 0; Gaps |
| Dd | 27 | LTVDSSSSPPIIEEEKTORFPDGAPPPFNLAADIRAAIPKHCWKPNPKMSYVRELAIV 86 |
| Qy | 1 | LTVDSSSSPPIIEEEKTORFPDGARPPFNLAADIRAAIPKHCWKPNPKMSYVRELAIV 60 |
| | | |
| Dd | 87 | FALAGAAYLNMLVLPPLWTIAOGTMTAFVLGHDGCGSFSDNRLNSVYGHLHSSI 144 |
| Qy | 61 | FALAGAAALNNMVLWPLWTIAOGTMETAFVLGHDCGHSFSNDPRLNSVYGHLHSSI 126 |
| | | |
| Dd | 147 | LVTYHHWRISRHTTHQNNGHYENDESMHPMSSEKIYKSLOKPTRFFFTFLPYMLAIPPYL 204 |
| Qy | 121 | LVTYHHWRISRHTTHQNNGHYENDESMHPMSSEKIYKSLOKPTRFFFRFTLPLVMLAPPYL 180 |
| | | |
| Dd | 207 | WAESPCKSKSHNPSPDFLPKRENDVLTSTACTATAVLLVCNLNVMPGMOMLKLVIYP 264 |
| Qy | 181 | WAESPCKSKSHNPSPDFLPKRENDVLTSTACTATAVLLVCNLNVMPGMOMLKLVIYP 244 |
| | | |
| Dd | 267 | YWINVMALDFVTYLHHHGHEDKLPWYRGKEMSYLRGSLTTLDROYGLINNHHDIGTHVI 324 |
| Qy | 241 | YWINVMALDFVTYLLHHHGHEDKLPWYRGKEMSYLRGSLTTLDROYGLINNHHDIGTHVI 300 |
| | | |
| Dd | 327 | NHLEFPDIPIHYHVEATEAKAVLYLGKYTRRDPKSGPLPLHLGLILASIKEDHFVSDEGDV 384 |
| Qy | 301 | NHLEFPDIPIHYHVEATEAKAVLYLGKYRRDPKSGPLPLHLGLILASIKEDHFVSDEGDV 360 |
| | | |
| Dd | 387 | VYYEADPNLYGEIKVTAE 404 |
| Qy | 361 | VYTEADPNLYGEIKVTAE 378 |
| | | |
| RESULT | 3 | |
| ID | PCT-US94-01321-10 | STANDARD; PRT; 446 AA. |
| XX | AC | xxxxxx |
| XX | DT | |
| XX | DE | |
| Sequence | 10, Application PC/TUS9401321 | |
| GENERAL INFORMATION: | | |
| APPLICANT: | | |
| TITLE OF INVENTION: | Altered Linolenic and Linoleic Acid Content | |
| TITLE OF INVENTION: | In Plants | |
| NUMBER OF SEQUENCES: | 72 | |
| COMPUTER READABLE FORM: | | |
| MEDIUM TYPE: | IBM PC compatible | |
| OPERATING SYSTEM: | PC-DOS/MS-DOS | |
| SOFTWARE: | PatentIn Release #1.0, Version #1.25 (EPO) | |
| CURRENT APPLICATION DATA: | | |
| APPLICATION NUMBER: | PCT/US94/01321 | |
| FILING DATE: | 04-FEB-1994 | |

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SQ
Query Match 27.2%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.67e-156;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 307 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTRDYGLINNHHDIGTH 366
OY 239 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTRDYGLINNHHDIGTH 298
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHTL 409
OY 299 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHTL 341
RESULT 4
ID PCT-US92-10284-5 STANDARD; PRT: 446 AA.
AC xxxxxx
XX
XX
XX
XX
DE Sequence 5, Application PC/TUS9210284
CC
CC Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SQ
Query Match 27.2%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 4.67e-156;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 307 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTRDYGLINNHHDIGTH 366
OY 239 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTRDYGLINNHHDIGTH 298
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHTL 409
OY 299 VIHHLFPOIPHYHLVEATEAKPVLGKYRPPDKSGPLPHTL 341
RESULT 5
ID PCT-US94-01321-12 STANDARD; PRT: 435 AA.
AC xxxxxx
XX
XX
XX
XX
DE Sequence 12, Application PC/TUS9401321
CC
CC Sequence 12, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 435 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 435 AA; 50136 MW; 1054240 CN;
SQ
Query Match 11.4%; Score 43; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.67e-55;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 349 INNHHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKYREP 391
OY 288 INNHHHDIGTHVHHLFPOIPHYHLVEATEAKPVLGKYREP 330
RESULT 6
ID PCT-US92-10284-13 STANDARD; PRT: 453 AA.
AC xxxxxx
XX
XX
XX
XX
DT

XX Sequence 13, Application PC/TUS9210284
DE
XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC
CC TELEEX: 835420
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 453 AA; 51362 MW; 1146882 CN;
SQ
Query Match 9.5%; Score 36; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.66e-43;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 327 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 362
QY 251 VTYLHHGHEDKLPYRGKESYLRGGLTTLDRDYG 286
RESULT 7
ID PCT-US92-10284-17 STANDARD: PRT; 156 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 17, Application PC/TUS9210284
XX
CC Sequence 17, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC

CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC
CC TELEEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFadk-2 and pYacp7
CC SEQUENCE 156 AA; 17771 MW; 128823 CN;
SQ
Query Match 8.2%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.06e-35;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 126 GHLSHSILVYHGWRIHSRTHHONGHVEN 156
QY 113 GHLSHSILVYHGWRIHSRTHHONGHVEN 143
RESULT 8
ID PCT-US94-01321-2 STANDARD: PRT; 383 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application PC/TUS9401321
XX
CC Sequence 2, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: PC-DOS/MS-DOS
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC

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CC CLASSIFICATION:  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/156551  
CC FILING DATE: 22-NOV-1993  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/014431  
CC FILING DATE: 05-FEB-1993  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 383 amino acids  
CC TYPE: amino acid  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 383 AA; 43936 MW; 846574 CN;  
SQ  
  
Query Match 7.4%; Score 28; DB 3; Length 383;  
Best Local Similarity 100.0%; Pred. No. 1,31e-30;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Db 123 ILVPYHGWIRISHRTHQNHGHVENDESW 150  
OY 120 ILVPYHGWIRISHRTHQNHGHVENDESW 147  
  
RESULT 9 STANDARD: PRT; 386 AA.  
ID PCF-US92-10284-2  
AC xxxxxx  
XX  
DT  
Sequence 2, Application PC/TUS9210284 .  
XX  
DE  
Sequence 2, Application PC/TUS9210284 .  
CC  
GENERAL INFORMATION:  
CC APPLICANT: Browne, John; Kinney, Anthony J.,  
CC APPLICANT: Pierce, John; Wierzbicki, Anna M.,  
CC APPLICANT: Yadev, Narendra S.; Perez-Grau, Luis  
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes  
CC FROM PLANTS  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: E. I. du Pont de Nemours and Company  
CC STREET: 1007 Market Street  
CC CITY: Wilmington  
CC STATE: Delaware  
CC COUNTRY: U.S.A.  
CC ZIP: 19898  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: Macintosh  
CC OPERATING SYSTEM: Macintosh System, 6.0  
CC SOFTWARE: Microsoft Word, 4.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCF/US92/10284  
CC FILING DATE: 19921203  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 07/804,259  
CC FILING DATE: 4 DECEMBER 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Floyd, Linda A.  
CC REGISTRATION NUMBER: 33,692  
CC REFERENCE/DOCKET NUMBER: BB-1036-A  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (302) 992-4929  
CC TELEFAX: (302) 892-7949  
CC TELEX: 835420  
CC INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 386 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: linear
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| CC | SEQUENCE | MOLECULE TYPE: protein | 386 AA; 44076 MW; 854247 CN; |
|----|---|-----------------------------------|------------------------------|
| CC | Query Match | 7.4%; Score 28; DB 3; Length 386; | |
| CC | Best Local Similarity 100.0%; Pred. No. 1,31e-30; | | |
| CC | Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| DB | 126 ILVPHGWRISRHRTHONHGHVENDSEW 153 | | |
| QY | 120 ILVPHGWRISRHRTHONHGHVENDSEW 147 | | |
| CC | RESULT 10 | | |
| CC | ID PCT-US92-10284-11 | STANDARD; | PRT; 380 AA. |
| CC | AC xxxxxx | | |
| CC | XX | | |
| CC | DT | | |
| CC | XX | | |
| DE | Sequence 11, Application PC/TUS9210284 | | |
| XX | | | |
| CC | Sequence 11, Application PC/TUS9210284 | | |
| CC | GENERAL INFORMATION: | | |
| CC | APPLICANT: Browne, John, Kinney, Anthony J., | | |
| CC | APPLICANT: Pierce, John, Wierzdicki, Anna W., | | |
| CC | APPLICANT: Yaday, Narendra S., Perez-Grau, Luis | | |
| CC | TITLE OF INVENTION: Fatty Acid Desaturase Genes | | |
| CC | TITLE OF INVENTION: from plants | | |
| CC | NUMBER OF SEQUENCES: 32 | | |
| CC | CORRESPONDENCE ADDRESS: | | |
| CC | ADDRESSEE: E. I. du Pont de Nemours and Company | | |
| CC | STREET: 1007 Market Street | | |
| CC | CITY: Wilmington | | |
| CC | STATE: Delaware | | |
| CC | COUNTRY: U.S.A. | | |
| CC | ZIP: 19898 | | |
| CC | COMPUTER READABLE FORM: | | |
| CC | MEDIUM TYPE: Floppy disk | | |
| CC | COMPUTER: Macintosh | | |
| CC | OPERATING SYSTEM: Macintosh System, 6.0 | | |
| CC | SOFTWARE: Microsoft Word, 4.0 | | |
| CC | CURRENT APPLICATION DATA: | | |
| CC | APPLICATION NUMBER: PCT/US92/10284 | | |
| CC | FILING DATE: 19921203 | | |
| CC | CLASSIFICATION: 435 | | |
| CC | Prior Application DATA: | | |
| CC | APPLICATION NUMBER: 07/804, 259 | | |
| CC | FILING DATE: 4 DECEMBER 1991 | | |
| CC | ATTORNEY/AGENT INFORMATION: | | |
| CC | NAME: Floyd, Linda A. | | |
| CC | REGISTRATION NUMBER: 33,692 | | |
| CC | REFERENCE/DOCKET NUMBER: BB-1036-A | | |
| CC | TELECOMMUNICATION INFORMATION: | | |
| CC | TELEPHONE: (302) 992-4925 | | |
| CC | TELEFAX: (302) 892-7949 | | |
| CC | TELEX: 835420 | | |
| CC | INFORMATION FOR SEQ ID NO: 11: | | |
| CC | SEQUENCE CHARACTERISTICS: | | |
| CC | LENGTH: 380 amino acids | | |
| CC | TYPE: AMINO ACID | | |
| CC | TOPOLOGY: linear | | |
| CC | MOLECULE TYPE: protein | | |
| CC | SEQUENCE 380 AA; 44185 MW; 827651 CN; | | |
| CC | SEQUENCE 380 AA; 44185 MW; 827651 CN; | | |
| CC | Query Match | 7.1%; Score 27; DB 3; Length 380; | |
| CC | Best Local Similarity 100.0%; Pred. No. 5.11e-29; | | |
| CC | Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | |
| DB | 295 NIHHDIGTHVHNLHPOLPHYHLYEAT 321 | | |
| QY | 290 NIHHDIGTHVHNLHPOLPHYHLYEAT 316 | | |

RESULT 11
ID US-08-320-982-6 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
DE Sequence 6, Application US/08320982
XX
CC Sequence 6, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KORULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.46e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFPOIPHYHLEAT 25
OY 292 HHDIQTHVHHLFPOIPHYHLEAT 316
RESULT 12
ID US-08-320-982-22 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
DE Sequence 22, Application US/08320982
XX
CC Sequence 22, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KORULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 7.46e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFPOIPHYHLEAT 25
OY 292 HHDIQTHVHHLFPOIPHYHLEAT 316
RESULT 13
ID US-08-314-596-6 STANDARD; PRT; 37 AA.
AC xxxxxx
XX
DT
DE Sequence 6, Application US/08314596
XX
CC Sequence 6, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005


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CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC
CC SEQUENCE 37 AA: 4331 MW: 8403 CN:
SQ
Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7,466-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 HHDTGTHVHHLPQIPHYHLYEAT 25
OY 292 HHDTGTHVHHLPQIPHYHLYEAT 316
RESULT 14
ID US-08-314-596-22 STANDARD: PRT; 37 AA.
XX AC xxxxxx
XX DT
XX
XX Sequence 22, Application US/08314596
DE
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

```

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CC          TELEFAX: 202-822-0944
CC          INFORMATION FOR SEQ ID NO: 22:
CC          SEQUENCE CHARACTERISTICS:
CC              LENGTH: 37 amino acids
CC              TYPE: amino acid
CC              STRANDEDNESS: single
CC              TOPOLOGY: linear
CC          MOLECULE TYPE: peptide
CC          SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match      6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 7,46e-26;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db
1 HHDIGTIVHHLPQIPHYHLVEAT 25
|||||
QY 292 HHDIGTIVHHLPQIPHYHLVEAT 316
|||||
RESULT 15
ID US-08-314-596-16 STANDARD; PRT; 37 AA.
XX
XX xxxxxx
DT
XX
XX
XX
XX
XX Sequence 16, Application US/08314596
DE
CC Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSSEE: CUSHMAN DAREY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4407 MW; 7119 CN;
SQ
Query Match      5.8%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 3,68e-21;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db
1 HHDIGTIVHHLPQIPHYHLV 22

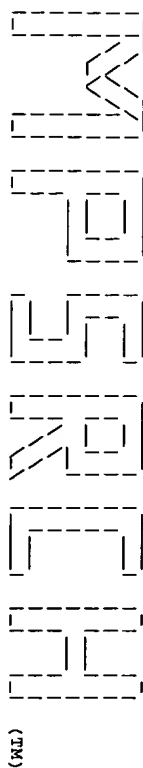
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|||||
Qy 292 HHDI GTVH HLEPQI PHXHLV 313

Search completed: Sat Aug 21 12:26:46 1999
Job time : 17 secs.



6
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Distribution rights by Oxford Molecular Ltd

Msearch - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:31:25 1999; Maspar time 16.73 Seconds
Tabular output not generated. 967.513 Million cell updates/sec

Title: >US-09-219-935-9
Description: (1-404) from US09219935.pep
Perfect Score: 404
Sequence: 1 EFKRQSPSPFRFLNSRNMA.....DVYYEADPNLGEIKVTAE 404

Scoring table: TABLE uniprottable
Gap 60

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: plr60
1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 3.655; Variance 0.462; scale 7.903

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|-------|-------------|------------------------|
| 1 | 404 | 100.0 | 404 | 2 | P00812 | omega-3 fatty acid de |
| 2 | 103 | 25.5 | 446 | 2 | J02336 | omega-3 fatty acid de |
| 3 | 43 | 10.6 | 398 | 2 | T01696 | omega-3 fatty acid de |
| 4 | 40 | 9.9 | 441 | 2 | T03029 | omega-3 fatty acid de |
| 5 | 36 | 8.9 | 443 | 2 | T01697 | omega-3 fatty acid de |
| 6 | 36 | 8.9 | 453 | 2 | J02339 | omega-3 fatty acid de |
| 7 | 28 | 6.9 | 377 | 2 | J02337 | omega-3 fatty acid de |
| 8 | 28 | 6.9 | 383 | 2 | A44227 | omega-3 fatty acid de |
| 9 | 28 | 6.9 | 386 | 2 | J02335 | omega-3 fatty acid de |
| 10 | 27 | 6.7 | 380 | 2 | J02338 | omega-3 fatty acid de |
| 11 | 24 | 5.9 | 379 | 2 | J02555 | omega-3 fatty acid de |
| 12 | 16 | 4.0 | 359 | 2 | S52650 | omega-3 fatty acid de |
| 13 | 8 | 2.0 | 326 | 2 | H71349 | probable ribosomal pr |
| 14 | 8 | 2.0 | 598 | 2 | S65770 | maltooligosyltrehalos |
| 15 | 8 | 2.0 | 1117 | 2 | S63399 | probable membrane pro |
| 16 | 7 | 1.7 | 112 | 2 | A25458 | neuropeptide L5 precu |
| 17 | 7 | 1.7 | 113 | 2 | A60887 | synuclein - Pacific e |
| 18 | 7 | 1.7 | 213 | 2 | S08313 | abscisic acid-induced |
| 19 | 7 | 1.7 | 224 | 2 | S16259 | embryonic abundant pr |
| 20 | 7 | 1.7 | 232 | 2 | D70754 | hypothetical protein |
| 21 | 7 | 1.7 | 249 | 2 | S78186 | H+-transporting ATP s |
| 22 | 7 | 1.7 | 299 | 2 | T00774 | hypothetical protein |
| 23 | 7 | 1.7 | 305 | 2 | A70212 | conserved hypothetical |

| | | | | | | | |
|----|---|-----|------|---|--------|------------------------|----------|
| 24 | 7 | 1.7 | 317 | 2 | S55316 | mucin (clone PGM-2B) | 4.35e+00 |
| 25 | 7 | 1.7 | 337 | 2 | A54214 | pentanene synthase | 4.35e+00 |
| 26 | 7 | 1.7 | 338 | 2 | F69437 | hypothetical protein | 4.35e+00 |
| 27 | 7 | 1.7 | 342 | 2 | E70463 | conserved hypothetical | 4.35e+00 |
| 28 | 7 | 1.7 | 367 | 1 | W0H0 | alpha-2-HS-glycoprote | 4.35e+00 |
| 29 | 7 | 1.7 | 371 | 1 | J06186 | transcription factor | 4.35e+00 |
| 30 | 7 | 1.7 | 388 | 2 | F69536 | alanine racemase (EC | 4.35e+00 |
| 31 | 7 | 1.7 | 392 | 2 | A30100 | conserved hypothetical | 4.35e+00 |
| 32 | 7 | 1.7 | 415 | 1 | C64473 | serine proteinase eas | 4.35e+00 |
| 33 | 7 | 1.7 | 447 | 2 | E64495 | adenosylhomocystein | 4.35e+00 |
| 34 | 7 | 1.7 | 447 | 2 | Q0BHS | hypothetical protein | 4.35e+00 |
| 35 | 7 | 1.7 | 488 | 1 | J07295 | alkaline exonuclease | 4.35e+00 |
| 36 | 7 | 1.7 | 528 | 2 | I47141 | gastric mucin (clone | 4.35e+00 |
| 37 | 7 | 1.7 | 533 | 2 | T01535 | probable cytochrome P | 4.35e+00 |
| 38 | 7 | 1.7 | 555 | 2 | I51671 | Weila kinase - Africa | 4.35e+00 |
| 39 | 7 | 1.7 | 674 | 2 | S75662 | hypothetical protein | 4.35e+00 |
| 40 | 7 | 1.7 | 674 | 2 | S75662 | sensory transduction | 4.35e+00 |
| 41 | 7 | 1.7 | 755 | 2 | B41836 | amine oxidase (flavin | 4.35e+00 |
| 42 | 7 | 1.7 | 1065 | 2 | E69795 | acriflavin resistance | 4.35e+00 |
| 43 | 7 | 1.7 | 1132 | 2 | S37932 | hypothetical protein | 4.35e+00 |
| 44 | 7 | 1.7 | 1944 | 2 | A55117 | tsq24 protein - mouse | 4.35e+00 |
| 45 | 7 | 1.7 | 2038 | 2 | A43742 | female sterile homeot | 4.35e+00 |

ALIGNMENTS

RESULT 1
ENTRY P00812 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999

ACCESSIONS P00812
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#contents CDNA:BND
#accession P00812
#molecule_type mRNA
#residues 1-404 #label YAD
##cross-references GB:I22963

COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400

Query Match 100.0%; Score 404; DB 2; Length 404;
Best local similarity 100.0%; Pred. No. 0.00e+00;

Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | | | | |
|----|-----|---------------------|------------|-----------|--------|--------|---------|-----|
| Db | 1 | EFKRQSPSPFRFLNSRNMA | NTTPTLVDS | SSSPLEEPK | TFQRP | PGAP | PNLADIR | 60 |
| Qy | 1 | EFKRQSPSPFRFLNSRNMA | LVNTTPTLV | DSSSPLEEP | KTRQRP | PGAP | PNLADIR | 60 |
| Db | 61 | AAIPKHCWVKNPKMSKYV | RELAIVFALA | GAAYLN | NMTLV | WPLYTA | OGTMT | 120 |
| Qy | 61 | AAIPKHCWVKNPKMSKYV | RELAIVFALA | GAAYLN | NMTLV | WPLYTA | OGTMT | 120 |
| Db | 121 | HDGCHGFSNDPR | NSVGHLL | SSITVPH | GMRTSR | THHNGH | ENESHP | 180 |
| Qy | 121 | HDGCHGFSNDPR | NSVGHLL | SSITVPH | GMRTSR | THHNGH | ENESHP | 180 |
| Db | 181 | YKSIDKPTREFR | FTLPLV | MLAYPP | YLWARS | PGKSGH | YHPD | 240 |
| Qy | 181 | YKSIDKPTREFR | FTLPLV | MLAYPP | YLWARS | PGKSGH | YHPD | 240 |

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Db 241 TAAVLLVLCNFMFGMOMKLTIVPYNTNMVLDFTVYLHHGHEDKLPYRGKEMSYL 300
Oy 241 TAAVALLVCNFMFGMOMKLTIVPYNTNMVLDFTVYLHHGHEDKLPYRGKEMSYL 300
Db 301 RGGITLDRDYGILNNIHHDIGTVIHHLPPIPHYLVEATEAKPVLGKYREPPDKSG 360
Oy 301 RGGITLDRDYGILNNIHHDIGTVIHHLPPIPHYLVEATEAKPVLGKYREPPDKSG 360
Db 361 PLPLHLGLIAKSIKEDHFVSDGDVYVYEAADPNLXGKRYVAE 404
Oy 361 PLPLHLGLIAKSIKEDHFVSDGDVYVYEAADPNLXGKRYVAE 404

RESULT 2
ENTRY JQ2336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
#cross
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSION JQ2336
REFERENCE JQ2335 A49503
#authors Yadau, N.S.; Mierzwicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#accession JQ2336
#molecule_type mRNA
#residues 446 #label YAD
REFERENCE A49503
#authors Iba, K.; Gibson, S.; Nishituchi, T.; Fuse, T.; Nishimura, M.;
Arondel, V.; Hugly, S.; Somerville, C.
#journal J. Biol. Chem. (1993) 268:24099-24105
#title A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and
chloroplast copy number of the fad7 mutant of Arabidopsis
thaliana.
#cross-references M01D:94043239
#accession A49503
#status preliminary
#molecule_type DNA
#residues 1-446 #label IBA
#cross-references GB:D14007; NID:9461160; PID:d1003612; PID:9541653
#note sequence extracted from NCBI backbone (NCBI:139485,
NCBIP:139486)
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
#superfamily omega-3 fatty acid desaturase
CLASSIFICATION #superfamily oxidoreductase
KEYWORDS #length 446 #molecular-weight 51174 #checksum 4653
SUMMARY
Query Match 25.5%: Score 103; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. NO.2.64e-297;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPYINVMWLDFTVYLHHGHEDKLPYRGKEMSYLGGITLDRDYGILNNIHHDIGTH 366
Oy 265 IPYINVMWLDFTVYLHHGHEDKLPYRGKEMSYLGGITLDRDYGILNNIHHDIGTH 324
Db 367 VINHLFPOIPHYHLVEATEAKPVLGKYREPPDKSGPLRLHL 409
Oy 325 VINHLFPOIPHYHLVEATEAKPVLGKYREPPDKSGPLRLHL 367

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ENTRY TITLE T01696 #type fragment
ORGANISM #formal_name zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
ACCESSIONS #journal (fragment)
REFERENCE #authors #formal_name zea mays #common_name maize
#title 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
#accession T01696
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-398 #label BER
#cross_references EMBL:D63953; NID:d1164452; PID:d1023305
#experimental_source strain honey bantum
GENETICS
#gene FAD8
KEYWORDS oxidoreductase
SUMMARY #length 398 #checksum 5580
Query Match 10.6%; Score 43; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,40e-102;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRGGLTTLDRDYGILNNHHIDIGTHVHHLFPQIPHYHL 333
296 EMSYLRGGLTTLDRDYGILNNHHIDIGTHVHHLFPQIPHYHL 338
|||||
|||||

RESULT 4 #type complete
ENTRY omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common
TITLE tobacco
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
T03029
T03029 #length 441 #molecular_weight 50310 #checksum 6941
#accession T03029
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross_references EMBL:D79979; NID:d1093316; PID:g1694625
#experimental_source cultivar SRL
GENETICS
#gene FAD7
KEYWORDS #superfamily omega-3 fatty acid desaturase
SUMMARY oxidoreductase
#length 441 #molecular_weight 50310 #checksum 6941

Db 355 INNTHHDIGTHVHHLFPQIPHYHLVATPAKPVLGKYY 394
314 INNTHHDIGTHVHHLFPQIPHYHLVATPAKPVLGKYY 353
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|||||

Query Match 9.9%; Score 40; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.70e-92;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5 #type complete
ENTRY omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
TITLE #formal_name zea mays #common_name maize
ORGANISM 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
DATE 19-Feb-1999

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ACCESSIONS T01697
REFERENCE Z14400
#authors Beberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
#journal Kusano, T.
#title Plant Mol. Biol. (1998) 36:297-306
#accession Two maize genes encoding omega-3 fatty acid desaturase and
#status their differential expression to temperature.
#molecule_type DNA
#residues Preliminary; translated from GB/EMBL/DBJ
#cross-references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantum

GENETICS
#gene FAD7
#introns 163/2: 193/2; 215/3: 246/3; 308/3: 335/3; 381/3
#exons oxidoreductase
#length 443 #molecular-weight 49437 #checksum 8872

KEYWORDS
SUMMARY

Query Match 8.9%; Score 36; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.88e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGHEDKLPWYRGKESYLRLGGLTTLDRDYG 352
|||
QY 277 VTYLHHGHEDKLPWYRGKESYLRLGGLTTLDRDYG 312

RESULT 6
ENTRY JQ2339 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
#formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS JQ2339
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
#molecule_type mRNA
#residues 1-453 #label YAD
#cross-references GB:L22965; NID:9408791; PID:9408792
#experimental_source third double bond in the biosynthesis of
#note 18:2 and 18:3 fatty acids which are important constituents of
#note plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 8.9%; Score 36; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.88e-80;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 327 VTYLHHGHEDKLPWYRGKESYLRLGGLTTLDRDYG 362
|||
QY 277 VTYLHHGHEDKLPWYRGKESYLRLGGLTTLDRDYG 312

RESULT 7
ENTRY JQ2337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
#formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BN3
#accession JQ2337
#molecule_type mRNA
#residues 1-377 #label YAD
#cross-references GB:L22962; NID:9408491; PID:9408492
#experimental_source third double bond in the biosynthesis of
#note 18:2 and 18:3 fatty acids which are important constituents of
#note plant membranes.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 6.9%; Score 28; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 ILVYHGMRIISHRTNHNHGHVNDSEW 144
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QY 146 ILVYHGMRIISHRTNHNHGHVNDSEW 173

RESULT 8
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
#formal_name Brassica napus #common_name rape
#cross-references MUID:94302147
#cross-references MUID:93088059
#accession A44227
#molecule_type nucleic acid
#residues 1-383 #label ARO
#cross-references GB:L01418; NID:9167147; PID:9167148
#experimental_source sequence extracted from NCBI backbone (NCBIP:119842)
#note Map-based cloning of a gene controlling omega-3 fatty acid
#note desaturation in Arabidopsis.

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 6.9%; Score 28; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 123 ILVYHGMRIISHRTNHNHGHVNDSEW 150
|||
QY 146 ILVYHGMRIISHRTNHNHGHVNDSEW 173

RESULT 9
ENTRY JQ2335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
#cross Arabidopsis thaliana
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
12-Mar-1999

ACCESSIONS JQ2335;
REFERENCE T02487

REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#accession J02335
#molecule_type mRNA
#residues 1-386 ##label YAD

REFERENCE J14675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.

#submission Submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23F1 genomic
#accession T02487
#status Translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-386 ##label ROU

COMMENT ##cross-references EMBL:NC004680; NID:g3420043; PID:g3420053
The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23F1.10

CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 6.9%; Score 28; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.31e-55;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 ILVPHGMRISHRTHQNHGHNDESW 153
|||
QY 146 ILVPHGMRISHRTHQNHGHNDESW 173

RESULT 10
ENTRY J02338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GM3 - soybean
ORGANISM #formal_name glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS J02338
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#accession J02338
#molecule_type mRNA
#residues 1-380 ##label YAD

COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
#superfamily omega-3 fatty acid desaturase
oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659

Query Match 6.7%; Score 27; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.29e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NHHHDIGTHVHHLFPOIPHYHLEAT 321
|||
QY 316 NHHHDIGTHVHHLFPOIPHYHLEAT 342

RESULT 11
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998

ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references M01D:95011632
#accession JC2555
#status Preliminary
#molecule_type mRNA
#residues 1-379 ##label HAM

COMMENT ##cross-references DBJ:D26509; NID:g1311480; PID:d1006059; PID:g599592
#superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular-weight 44149 #checksum 1940

Query Match 5.9%; Score 24; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 9.77e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 NHHHDIGTHVHHLFPOIPHYH 314
|||
QY 315 NHHHDIGTHVHHLFPOIPHYH 338

RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synecocystis
sp. (strain PCC6803)
ALTERNATE_NAMES delta 15 desaturase
ORGANISM #formal_name Synecocystis sp.
#variety PCC 6803
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999

ACCESSIONS S52650; S75843
REFERENCE S52649
#authors Sakamoto, T.; Los, D.A.; Higaishi, S.; Wada, H.; Nishida, I.;
Ohmori, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from cyanobacteria and its use
in altering the degree of membrane-lipid unsaturation.
#cross-references M01D:95035996
#accession S52650
#molecule_type DNA
#residues 1-359 ##label SAK
##cross-references GB:D13780; NID:g600596; PID:d1003430; PID:g600598
##note The authors translated the initiation codon GTG for
residue 1 as Val

REFERENCE S74322
#authors Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shingo,
S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synecocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of

```

#cross-references MIMD:97061201          potential protein-coding regions
#accession      575843
##status
##molecule_type DNA
##residues      1-359 ##label KAN
##cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035
                        P1D:g1653388
##note
                        the nucleotide sequence was submitted to the EMBL Data
                        Library, June 1996

GENETICS
#start_codon      GTG
CLASSIFICATION      #superfamily omega-3 fatty acid desaturase
KEYWORDS            #oxidoreductase
SUMMARY             #length 359 #molecular-weight 41919 #checksum 9162

Query Match      4.0%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3,77e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      114 ILVPHYHGMRIISHRTTH 129
      |||||||
QY      146 ILVPHYHGMRIISHRTTH 161

RESULT      13
ENTRY        H71349          #type complete
TITLE        Probable ribosomal protein L1 (rplA) - syphilis spirochete
ORGANISM      #formal_name Treponema pallidum subsp. pallidum #common_name
               syphilis spirochete
DATE          24-Jul-1998 #sequence_rev1sion 24-Jul-1998 #text_change
               17-Mar-1999

ACCESSIONS
REFERENCE      H71349
               A71250
               Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.;
               Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.K.; Clayton
               R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
               M.P.; Salzberg, S.; Peterson, J.; Khair, H.; Richardson,
               D.; Howell, J.K.; Chidambaram, M.; Ueberback, T.; McDonald
               L.; Artlich, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
               Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Matthey,
               L.; Weidman, J.; Smith, H.O.; Venter, J.C.
               Science (1998) 281:375-388
               Complete genome sequence of Treponema pallidum, the syphilis
               spirochete.
               #cross-references MIMD:98332770
               #accession      H71349
               #status      preliminary: nucleic acid sequence not shown;
               translation not shown

##molecule_type DNA
##residues      1-226 ##label COL
##cross-references GB:AE001205; GB:AE000520; NID:g3322501; PID:g3322508
##experimental_source strain Nichols

GENETICS
#gene      TP0238
CLASSIFICATION      #superfamily Escherichia coli ribosomal protein L1
SUMMARY             #length 226 #molecular-weight 24977 #checksum 6350

Query Match      2.0%; Score 8; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 5.98e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db      83 ALAAGAY 90
      |||||
QY      88 ALAAGAY 95

RESULT      14
ENTRY        S65770          #type complete
TITLE        malcoo1igoyltrehalose trehalohydrolase - Arthrobacter sp.
               (strain Q36)
ORGANISM      #formal_name Arthrobacter sp.
               variety strain Q36

```

```

DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
18-Sep-1998

ACCESSIONS S65770
REFERENCE S65769
#authors Maruta, K.; Hattori, K.; Nakada, T.; Kubota, M.; Sugimoto,
T.; Kurimoto, M.
#journal Biochim. Biophys. Acta (1996) 1289:10-13
#title Cloning and sequencing of trehalose blosynthesis genes from
Arthrobacter sp. Q36.
#cross-references NCID:96195835
#accession S65770
#status preliminary
#molecule_type DNA
#residues 1-598 ##label MAR
#cross-references EMBL:D65343; NID:g1255444; PID:d1010313; PID:g1255446
CLASSIFICATION #superfamily_trehalose_trehalohydrolase
SUMMARY #length 598 #molecular-weight 65831 #checksum 4532

Query Match 2.0%; Score 8; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 5,98e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAAKPVLG 15
QY 343 EAAKPVLG 350

RESULT 15 S63399 #type complete
ENTRY probable membrane protein YNR067c - yeast (Saccharomyces
TITLE cerevisiae)
ALTERNATE_NAMES hypothetical protein N3547
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 27-Apr-1996 #sequence_revision 03-May-1996 #text_change
14-Nov-1997

ACCESSIONS S63399
REFERENCE S63944
#authors Duesterhoeft, A.; Floeth, M.; Fritze, C.; Heuss-Neitzel, D.;
Hilbert, R.; Moestl, D.
#submission submitted to the Protein Sequence Database, April 1996
#accession S63399
#molecule_type DNA
#residues 1-1117 ##label DUE
#cross-references EMBL:D71682; NID:g1302597; PID:e239600; PID:g1302598;
MIPS:YNR067C
#experimental_source strain S288C

GENETICS
#map_position 14R transmembrane protein
KEYWORDS FEATURE
6-22 #domain transmembrane #status predicted #label TM
SUMMARY #length 1117 #molecular-weight 121063 #checksum 7513

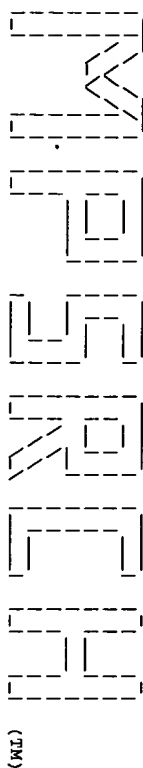
Query Match 2.0%; Score 8; DB 2; Length 1117;
Best Local Similarity 100.0%; Pred. No. 5,98e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 339 TVDSSSP 346
QY 28 TVDSSSP 35

Search completed: Sat Aug 21 12:32:25 1999
Job time : 60 secs.

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MPsrch-PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:32:42 1999; Maspar time 11.63 seconds

Tabular output not generated.

Title: >US-09-219-935-9
Description: (1-404) from US09219935.pep
Perfect Score: 404
Sequence: 1 FKFROSPSPFRFLNSRNMA.....DYYVYADNLTGEIKVTAE 404

Scoring table: TABLE unltprotable
Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 3.728; Variance 0.433; scale 8.613

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 404 | 100.0 | 404 | 1 | FD3C_BRANA OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 2 | 103 | 25.5 | 446 | 1 | FD3C_ARATH OMEGA-3 FATTY ACID DES | 0.00e+00 |
| 3 | 42 | 10.6 | 435 | 1 | FD3D_ARATH TEMPERATURE-SENSITIVE | 8.21e-111 |
| 4 | 42 | 10.4 | 460 | 1 | FD3C_RICCO OMEGA-3 FATTY ACID DES | 2.18e-107 |
| 5 | 36 | 8.9 | 447 | 1 | FD3C_SESIN OMEGA-3 FATTY ACID DES | 5.08e-87 |
| 6 | 36 | 8.9 | 453 | 1 | FD3C_SOYBN OMEGA-3 FATTY ACID DES | 5.08e-87 |
| 7 | 28 | 6.9 | 377 | 1 | FD31_BRANA OMEGA-3 FATTY ACID DES | 1.77e-60 |
| 8 | 28 | 6.9 | 383 | 1 | FD32_BRANA OMEGA-3 FATTY ACID DES | 1.77e-60 |
| 9 | 28 | 6.9 | 386 | 1 | FD3E_ARATH OMEGA-3 FATTY ACID DES | 1.77e-60 |
| 10 | 27 | 6.2 | 380 | 1 | FD3E_SOYBN OMEGA-3 FATTY ACID DES | 8.86e-51 |
| 11 | 25 | 6.2 | 379 | 1 | FD3E_PHAUV OMEGA-3 FATTY ACID DES | 3.17e-57 |
| 12 | 24 | 5.9 | 379 | 1 | FD3E_TOBAC OMEGA-3 FATTY ACID DES | 1.38e-47 |
| 13 | 24 | 5.9 | 379 | 1 | FD3E_TOBAC OMEGA-3 FATTY ACID DES | 1.38e-47 |
| 14 | 8 | 2.0 | 1117 | 1 | YNS6_YEAST HYPOTHETICAL 121.1 KD | 2.13e-02 |
| 15 | 7 | 1.7 | 85 | 1 | RLT7_STRGR 50S RIBOSOMAL PROTEIN | 2.13e-02 |
| 16 | 7 | 1.7 | 100 | 1 | CH10_THETH 10 KD CHAPERONIN (PROT | 2.06e+00 |
| 17 | 7 | 1.7 | 112 | 1 | AGN5_APLCA ABDOMINAL GANGLION NEU | 2.06e+00 |
| 18 | 7 | 1.7 | 143 | 1 | SVL_TORCA SYNDOLEIN | 2.06e+00 |
| 19 | 7 | 1.7 | 213 | 1 | LEAL_HORVU ABA-INDUCIBLE PROTEIN | 2.06e+00 |
| 20 | 7 | 1.7 | 232 | 1 | HYPOHETICAL 23.9 KD P | 2.06e+00 |
| 21 | 7 | 1.7 | 236 | 1 | LYSE_CORGL LYSINE EXPORTER PROTEI | 2.06e+00 |
| 22 | 7 | 1.7 | 280 | 1 | DUS7_RAT DUAL SPECIFICITY PROTE | 2.06e+00 |
| 23 | 7 | 1.7 | 322 | 1 | DUS7_HUMAN DUAL SPECIFICITY PROTE | 2.06e+00 |

| RESULT | 1 | STANDARD | PRT | 404 AA. | ALIGNMENTS |
|--------|--|----------|-----|---------|------------|
| ID | FD3C_BRANA | | | | |
| AC | P46618; | | | | |
| DT | 01-FEB-1996 (REL. 33, CREATED) | | | | |
| DT | 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) | | | | |
| DT | 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE) | | | | |
| DE | OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-) | | | | |
| DE | (FRAGMENT). | | | | |
| GN | FAD7. | | | | |
| OS | BRASSICA NAPUS (RAPE). | | | | |
| OC | EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; | | | | |
| OC | EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE; | | | | |
| OC | CAPRARALES; BRASSICACEAE; BRASSICA. | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=SEED; | | | | |
| FX | MEDLINE: 94302147. | | | | |
| RA | YANAV N.S., WIERZBICKI A., ABERGER M., CASTER C.S., PEREZ-GRU L., | | | | |
| RA | KINNEY A.J., HITZ R.D., BOOTH J.R. JR., SCHWETGER B., STECCA K.L., | | | | |
| RA | ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H., | | | | |
| RT | FELDMANN K.A., PIERCE J., BROWSE J.; | | | | |
| RL | "Cloning of higher plant omega-3 fatty acid desaturases."; | | | | |
| CC | PLANT PHYSIOL. 103:467-476(1993). | | | | |
| CC | -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES | | | | |
| CC | THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY | | | | |
| CC | ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT | | | | |
| CC | TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS | | | | |
| CC | ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. | | | | |
| CC | -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. | | | | |
| CC | -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY). | | | | |
| CC | -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONSTRAIN THE ACTIVE SITE | | | | |
| CC | AND/OR BE INVOLVED IN METAL ION BINDING. | | | | |
| CC | -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES. | | | | |
| CC | ----- | | | | |
| CC | This SWISS-PROT entry is copyright. It is produced through a collaboration | | | | |
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| CC | or send an email to license@isb-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL: L22963; G408490; ALT_INIT. | | | | |
| DR | PIR: P00812; P00812. | | | | |
| DR | PFAM: PF00487; FA_desaturase; 1. | | | | |
| KW | OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE; | | | | |
| KW | TRANSIT PEPTIDE. | | | | |

```

FT  NON_TER  1  1  CHLOROPLAST (POTENTIAL).
FT  TRANSIT  <1  ?  OMEGA-3 FATTY ACID DESATURASE,
FT  CHAIN    ?  404  CHLOROPLAST.
FT  DOMAIN   121  125  HISTIDINE BOX 1.
FT  DOMAIN   157  161  HISTIDINE BOX 2.
FT  DOMAIN   324  328  HISTIDINE BOX 3.
SO  SEQUENCE  404 AA: 46617 MW; 79719FB CRC32;

Query Match      100.0%; Score 404; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  1  EFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60
    1  FFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60
Oy  1  FFKRSPSSPRRLNSRMALVNTPLVDDSSPPREEPTQRPDGPAPPFNLADIR 60

Db  61  AAIPIHCWKNPKMSYVYRELATVFAAAGATLNNMLVPLVIAAGTFFALFVLG 120
    61  AAIPIHCWKNPKMSYVYRELATVFAAAGATLNNMLVPLVIAAGTFFALFVLG 120
Oy  61  AAIPIHCWKNPKMSYVYRELATVFAAAGATLNNMLVPLVIAAGTFFALFVLG 120

Db  121  HDGCGSFSNDRLNSVYGLHSSILVYHGMRIISHRTNHNHGVNDESMHPMSKTI 180
    121  HDGCGSFSNDRLNSVYGLHSSILVYHGMRIISHRTNHNHGVNDESMHPMSKTI 180
Oy  121  HDGCGSFSNDRLNSVYGLHSSILVYHGMRIISHRTNHNHGVNDESMHPMSKTI 180

Db  181  YKSLDKPTREFFRTPLVLAIPYLLMARSPPKSGSHVPSDLEFLPKERNDYLTSTACW 240
    181  YKSLDKPTREFFRTPLVLAIPYLLMARSPPKSGSHVPSDLEFLPKERNDYLTSTACW 240
Oy  181  YKSLDKPTREFFRTPLVLAIPYLLMARSPPKSGSHVPSDLEFLPKERNDYLTSTACW 240

Db  241  TMAVVLVCLNFMVGMOMLKLVIPIYVNVNMDVYTLHHNGHEDKLPWYRGKEMSTL 300
    241  TMAVVLVCLNFMVGMOMLKLVIPIYVNVNMDVYTLHHNGHEDKLPWYRGKEMSTL 300
Oy  241  TMAVVLVCLNFMVGMOMLKLVIPIYVNVNMDVYTLHHNGHEDKLPWYRGKEMSTL 300

Db  301  RGLTTLDRDYGLINNHHIDISTHYVHLFPQIPHYHLVEATEAKPVLYGKYRREPKSG 360
    301  RGLTTLDRDYGLINNHHIDISTHYVHLFPQIPHYHLVEATEAKPVLYGKYRREPKSG 360
Oy  301  RGLTTLDRDYGLINNHHIDISTHYVHLFPQIPHYHLVEATEAKPVLYGKYRREPKSG 360

Db  361  PPLHLGLILANSIKEDHFEVDEGDVYVYEADPNLYGEIKVTAE 404
    361  PPLHLGLILANSIKEDHFEVDEGDVYVYEADPNLYGEIKVTAE 404
Oy  361  PPLHLGLILANSIKEDHFEVDEGDVYVYEADPNLYGEIKVTAE 404

RESULT  2
ID  FD3C_ARATH  STANDARD:  PRT:  446 AA.
AC  P46310;
DT  01-NOV-1995 (REL. 32, CREATED)
DT  01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT  01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE  OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN  FAD3 OR FAD3.
OS  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC  CHLOROPLAST.
OC  EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC  EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC  CAPPARLES: BRASSICACEAE; ARABIDOPSIS.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL;
RX  MEDLINE: 94032147.
RA  YADAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA  KINNEY A.O., HITE W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA  ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA  FELDMAN R.A., PIERCE J., BROWSE J.;
RT  "Cloning of higher plant omega-3 fatty acid desaturases.";
RL  PLANT PHYSIOL. 103:467-476(1993).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLUMBIA: TISSUE-AERIAL PARTS;
RX  MEDLINE: 94043239.
RA  IBA K., GIBSON S., NISHUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA  HUGLY S., SOMERVILLE C.R.;
RT  "A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and chloroplast

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RT  copy number of the fad7 mutant of Arabidopsis thaliana.";
RL  J. BIOL. CHEM. 268:24099-24105(1993).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL;
RA  WATANIKI M., YAMAMOTO K.;
RL  SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC  -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC  THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC  ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC  TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC  ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC  -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC  -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC  -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC  -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC  AND/ OR BE INVOLVED IN METAL ION BINDING.
CC  -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC  -----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: L22961; G408481; -
DR  EMBL: D14007; G541653; -
DR  EMBL: D26019; G468434; -
DR  FRAM: PF00487; FA_desaturase; 1.
KW  OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW  TRANSIT PEPTIDE.
FT  TRANSIT  1  ?  CHLOROPLAST (POTENTIAL).
FT  CHAIN    ?  446  OMEGA-3 FATTY ACID DESATURASE,
FT  DOMAIN   163  167  HISTIDINE BOX 1.
FT  DOMAIN   199  203  HISTIDINE BOX 2.
FT  DOMAIN   366  370  HISTIDINE BOX 3.
SO  SEQUENCE  446 AA: 51174 MW; 8DE08779 CRC32;

Query Match      25.5%; Score 103; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  307  IPYWINVMDLVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDRDYGLINNHHIDISTH 366
    265  IPYWINVMDLVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDRDYGLINNHHIDISTH 324
Oy  265  IPYWINVMDLVYTLHHGHEDKLPWYRGKEMSTLRGLTTLDRDYGLINNHHIDISTH 324

Db  367  VIHHLFQIPHYHLVEATEAKPVLYGKYRREPKSGPPLHL 409
    325  VIHHLFQIPHYHLVEATEAKPVLYGKYRREPKSGPPLHL 367
Oy  325  VIHHLFQIPHYHLVEATEAKPVLYGKYRREPKSGPPLHL 367

RESULT  3
ID  FD3D_ARATH  STANDARD:  PRT:  435 AA.
AC  P48622;
DT  01-FEB-1996 (REL. 33, CREATED)
DT  01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT  01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE  TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE  PRECURSOR (EC 1.14.99.-).
GN  FAD8.
OS  ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC  EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC  EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC  CAPPARLES: BRASSICACEAE; ARABIDOPSIS.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CV. COLUMBIA: TISSUE-AERIAL PARTS;
RX  MEDLINE: 95148742.
RA  GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
RT  "Cloning of a temperature-regulated gene encoding a chloroplast

```

RT Omega-3 desaturase from *Arabidopsis thaliana*.
RL PLANT PHYSIOL. 106:1615-1621(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA: TISSUE-HYPOCOTYL;
RA WATANAKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: L27158; G516045; -
DR EMBL: U08216; G497219; -
DR EMBL: D17578; G471093; -
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT TRANSIT 1 2
FT CHAIN ? 435 CHLOROPLAST (POTENTIAL).
FT FT TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
FT DOMAIN 156 160 HISTIDINE BOX 1.
FT DOMAIN 192 196 HISTIDINE BOX 2.
FT DOMAIN 359 363 HISTIDINE BOX 3.
SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;

Query Match 10.6%; Score 43; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 8,21e-111;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHIDGTHVHHLPQIPHVLVEATEAKPVLGKTYREP 391
Y 314 INNHHIDGTHVHHLPQIPHVLVEATEAKPVLGKTYREP 356

RESULT 4
ID FD3C.RICCO STANDARD; PRT; 460 AA.
AC P48619;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7A-1.
OS RICINUS COMMUNIS (CASTOR BEAN).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE-SEED;
RA MEDLINE; 9430217.
RA VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from *Ricinus communis*."
RL PLANT PHYSIOL. 105:443-444(1994).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -----
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CC -----
DR EMBL: U25817; G870784; -
DR PFAM: PF00487; FA_desaturase; 1.

CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: L25897; G414732; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT TRANSIT 1 2
FT CHAIN ? 460 CHLOROPLAST (POTENTIAL).
FT FT OMEGA-3 FATTY ACID DESATURASE,
FT DOMAIN 177 181 HISTIDINE BOX 1.
FT DOMAIN 213 217 HISTIDINE BOX 2.
FT DOMAIN 380 384 HISTIDINE BOX 3.
SQ SEQUENCE 460 AA; 52561 MW; DB3DA689 CRC32;

Query Match 10.4%; Score 42; DB 1; Length 460;
Best Local Similarity 100.0%; Pred. No. 2,18e-107;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 190 LNSVGHLSHSILVPGHGRISHRTGHNGHNEDESWHP 231
Y 134 LNSVGHLSHSILVPGHGRISHRTGHNGHNEDESWHP 175

RESULT 5
ID FD3C.SESIN STANDARD; PRT; 447 AA.
AC P48620;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINNELLY).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALACEAE; SESAMUM.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. 4294; TISSUE-COTYLEDON;
RA SHOOT K.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: U25817; G870784; -
DR PFAM: PF00487; FA_desaturase; 1.

RESULT 8
ID F032_BRNA STANDARD: PRT: 383 AA.
AC P46624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUCHARYOTA: VIRIDIPHYTES: STREPTOPHYTES: EMBRYOPHYTES: TRACHEOPHYTES:
OC EUCHARYOTA: VIRIDIPHYTES: SPERMATOPHYTES: MAGNOLIOPHYTES: EUDICOTYLEDONS: ROSIDAE:
OC CAPPALES: BRASSICACEAE: BRASSICA.
RN
RP
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC
DR EMBL: L01418; G167148; -
DR PFM: PFM00487; FA:desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 98 102 HISTIDINE BOX 1.
FT DOMAIN 134 138 HISTIDINE BOX 2.
FT DOMAIN 301 305 HISTIDINE BOX 3.
SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;
Query Match 6.9%; Score 28; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.77e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 123 ILVPHGWRISHRTHQNHGVNDESW 150
QY 146 ILVPHGWRISHRTHQNHGVNDESW 173

CC CAPPALES; BRASSICACEAE; ARABIDOPSIS.
RN
RP
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICT A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITE W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHITI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RX MEDLINE: 94345020.
RA NISHICHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana.";
RL PLANT PHYSIOL. 105:767-768(1994).
RN
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA ROUNSLEY S.D., LIN X., KENCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA STYES S.M., NAUL S., MASON T.M., KERLAUGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
DR EMBL: L22931; G408483; -
DR EMBL: D17579; G471091; -
DR EMBL: D26508; G1197795; -
DR EMBL: AC004680; G3420053; -
DR PFM: PFM00487; FA:desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 220 240 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 101 105 HISTIDINE BOX 1.
FT DOMAIN 137 141 HISTIDINE BOX 2.
FT DOMAIN 304 308 HISTIDINE BOX 3.
SQ SEQUENCE 386 AA; 44076 MW; C22B4B8C CRC32;
Query Match 6.9%; Score 28; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.77e-60;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 ILVPHGWRISHRTHQNHGVNDESW 153

OY 146 ILVPHGWRISHRTHQNGHVENDESW 173
 ||||||||||||||||||
 RESULT 10
 ID FD3E_S0YBN STANDARD: PRT: 380 AA.
 AC P48625.
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
 GN FAD3.
 OS GLUCINE MAX (SOYBEAN).
 OC EUPHYLLIPHTES: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
 OC EUPHYLLIPHTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
 OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE: 94302147.
 RA YADAV N.S., WIERZICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ M.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: MICROSOML (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL: J22964; G408794; -.
 DR PIR: J02338; J02338.
 DR PFAM: PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 55 75 POTENTIAL.
 FT TRANSMEM 212 232 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 100 104 HISTIDINE BOX 1.
 FT DOMAIN 136 140 HISTIDINE BOX 2.
 FT DOMAIN 303 307 HISTIDINE BOX 3.
 FT SEQUENCE 380 AA; 44185 MW; E3C50987 CRC32;
 SQ
 Query Match 6.7%; Score 27; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 3.17e-57;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 295 NHHHDSHTVHHLFPOIPHYHLEAT 321
 OY 316 NHHHDSHTVHHLFPOIPHYHLEAT 342
 ||||||||||||||||||
 RESULT 11
 ID FD3E_PHAU STANDARD: PRT: 380 AA.
 AC P32291;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)

DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
 GN ARG1.
 OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
 OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
 OC EUPHYLLIPHTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
 OC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HYPOCOTYL;
 RX YANAMOTO K.T., MORI H., IMASEKI H.;
 RA "Novel mRNA sequences induced by indole-3-acetic acid in sections of
 RT elongating hypocotyls of mung bean (Vigna radiata).";
 RL PLANT CELL PHYSIOL. 33:13-20(1992).
 CC -1- FUNCTION: MICROSOML (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/ OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL: D14410; G287562; -.
 DR PFAM: PF00487; FA_desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 59 78 POTENTIAL.
 FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 FT SEQUENCE 380 AA; 43996 MW; 8429BF68 CRC32;
 SQ
 Query Match 6.2%; Score 25; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 8.86e-51;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 294 HHDHSTVHHLFPOIPHYHLEAT 318
 OY 318 HHDHSTVHHLFPOIPHYHLEAT 342
 ||||||||||||||||||
 RESULT 12
 ID FD3E_TOBAC STANDARD: PRT: 379 AA.
 AC P48626.
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
 GN FAD3.
 OS NICOTIANA TABACUM (COMMON TOBACCO).
 OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
 OC EUPHYLLIPHTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS;
 OC ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SR1; TISSUE=LEAF;
 RX MEDLINE: 95011632.

RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.:
"Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase,"
RL GENE 147:293-294(1994).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CITOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC
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CC
DR EMBL: D26509; G599592; -
DR PFM: PF00487; FA.desaturase; 1.
KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KM TRANSMEMBRANE.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 213 233 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 97 101 HISTIDINE BOX 1.
FT DOMAIN 133 137 HISTIDINE BOX 2.
FT DOMAIN 300 304 HISTIDINE BOX 3.
SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;

Query Match 5.9%; Score 24; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.38e-47;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 NHHHIGTHVHHLFPIPHYL 314
315 NHHHIGTHVHHLFPIPHYL 338
QY

RESULT 13
ID RL1 TREPA STANDARD; PRT: 226 AA.
AC 083266;
DT 15-DEC-1998 (REL. 37, CREATED)
DT 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE 50S RIBOSOMAL PROTEIN L1.
GN RPLA OR TP0238
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NICHOLS;
RX MEDLINE: 98332770.
RA PRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERREN E., HARHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
RL SCIENCE 281:375-384(1998).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIP FAMILY OF RIBOSOMAL PROTEINS.

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CC
DR EMBL: AE001205; G3322508; -
DR TIGR: TP0238; -
DR PROSITE: PS01199; RIBOSOMAL_L1; 1.
KM RIBOSOMAL PROTEIN; RNA-BINDING.
SQ SEQUENCE 226 AA; 24977 MW; 423DF8A1 CRC32;

Query Match 2.0%; Score 8; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.13e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 83 ALAAGAAY 90
88 ALAAGAAY 95
QY

RESULT 14
ID YN96_YEAST STANDARD; PRT: 1117 AA.
AC P53753;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 121.1 KD PROTEIN IN BIO3-HXT17 INTERGENIC REGION
DE PRECURSOR.
GN YNR067C OR N547.
OS SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCCHAROMYCETALES;
OC SACCCHAROMYCETACEAE; SACCCHAROMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RA DUESTERHOEF A., FLOETH M., FRITZ C., HEUSS-NETZEL D.,
RA HILBERT H., MOESTL D.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SIMILARITY: TO YEAST YLR144C AND S.POMBE SPAC23D3.10C.
CC
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CC
DR EMBL: Z71682; E239600; -
KM HYPOTHETICAL PROTEIN; GLYCOPROTEIN; SIGNAL.
FT SIGNAL 1 16
FT CHAIN 17 1117
FT DOMAIN 342 345
FT DOMAIN 365 370
FT DOMAIN 376 383
FT CARBOHYD 138 138
FT CARBOHYD 186 186
FT CARBOHYD 223 223
FT CARBOHYD 259 259
FT CARBOHYD 280 280
FT CARBOHYD 303 303
FT CARBOHYD 307 307
FT CARBOHYD 333 333
FT CARBOHYD 533 533
FT CARBOHYD 886 886
SQ SEQUENCE 1117 AA; 121063 MW; 9A5486C6 CRC32;

Query Match 2.0%; Score 8; DB 1; Length 1117;
Best Local Similarity 100.0%; Pred. No. 2.13e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 339 TVDSSSP 346
 |||||
 Oy 28 TVDSSSP 35

RESULT 15
 ID RI27_STRGR STANDARD: PRT: 85 AA.

AC P95737;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE 50S RIBOSOMAL PROTEIN L27.
 GN RPMA

OS STREPTOMYCES GRISEUS.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-IFO 13189;
 RX MEDLINE; 97136618.

RA OKAMOTO S., ITOH M., OCHI K.;

RT "Molecular cloning and characterization of the obp gene of
 RT Streptomyces griseus in relation to the onset of morphological
 RT differentiation.";

RL J. BACTERIOL. 179:170-179(1997).

CC -!- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.

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 CC -----

DR EMBL: D87916; G1783293; -.

DR PROSITE: PS00831; RIBOSOMAL_L27; 1.

DR PFM: PFO1016; Ribosomal_L27; 1.

RW RIBOSOMAL PROTEIN.

SO SEQUENCE 85 AA; 8860 MW; 804E9523 CRC32;

Query Match 1.7%; Score 7; DB 1; length 85;

Best Local Similarity 100.0%; Pred.No. 2.06e+00; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 FALAAGA 66
 |||||

Oy 87 FALAAGA 93

Search completed: Sat Aug 21 12:33:03 1999
 Job time : 21 secs.


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RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409: D1023307: -.
DR EMBL: D63953: D1023305: -.
DR FRAM: PF00487: FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA: 44789 MW: 705658EC CRC32:

Query Match 10.6% Score 43; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 1,44e-103;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 291 EMSYLRLGLTTLDRDYGLNNIHHDIGTHVHHLFPQIPHYHL 333
Oy 296 EMSYLRLGLTTLDRDYGLNNIHHDIGTHVHHLFPQIPHYHL 338

RESULT 3
ID 082068 PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; SOLANACEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ007739: E1318202: -.
SQ SEQUENCE 431 AA: 49253 MW: BAFAP9CD CRC32:

Query Match 9.9% Score 40; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 5,41e-94;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 345 INNIHHDIGTHVHHLFPQIPHYHLVEATEAKPVLGKRY 384
Oy 314 INNIHHDIGTHVHHLFPQIPHYHLVEATEAKPVLGKRY 353

RESULT 4
ID P93350 PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NTERAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANACEAE; SOLANACEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 96416423.
RA HANADA T., NISHIGUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RL "cDNA cloning of a wounding-inducible gene encoding a plastid omega-3
RT fatty acid desaturase from tobacco."
DR PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL: D79979: D1012141: -.

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DR FRAM: PF00487: FA_desaturase; 1.
DR MENDEL: 9312; Nicta:1208;2.
SQ SEQUENCE 441 AA: 50310 MW: 255F96A6 CRC32:

Query Match 9.9% Score 40; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 5,41e-94;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 355 INNIHHDIGTHVHHLFPQIPHYHLVEATEAKPVLGKRY 394
Oy 314 INNIHHDIGTHVHHLFPQIPHYHLVEATEAKPVLGKRY 353

RESULT 5
ID 004807 PRELIMINARY; PRT; 438 AA.
AC 004807;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FRUTESCENS.
OC EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIACEAE; PERILLA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OKDONG;
RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U554477: G1754795: -.
DR FRAM: PF00487: FA_desaturase; 1.
DR MENDEL: 16268; PERIT:1208;ml16268.
SQ SEQUENCE 438 AA: 50160 MW: EE726819 CRC32:

Query Match 9.2% Score 37; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 1,74e-84;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 GHLHSSILVYHGMRIHSHRTHONHGHVDESMWP 217
Oy 139 GHLHSSILVYHGMRIHSHRTHONHGHVDESMWP 175

RESULT 6
ID 023824 PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA, VIRIDIPLANTAE, STREPTOPHYTA, EMBRYOPHYTA, TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN=HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL "Two maize genes encoding omega-3 fatty acid desaturase and their
RT differential expression to temperature."
DR PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954: D1023306: -.
DR EMBL: D63952: D1023304: -.
DR FRAM: PF00487: FA_desaturase; 1.
SQ SEQUENCE 443 AA: 49437 MW: E8B6C757 CRC32:

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RA IRA K.;
RL PHYSIOL. PLANTARUM 96:275-283(1996).
DR EMBL; D43688; D1008371; -.
PFAM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;
Query Match 5.9%; Score 24; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.92e-44;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 130 GWRISHRTHQNHGHVDESMWP 153
152 GWRISHRTHQNHGHVDESMWP 175
RESULT 12
ID 055240 PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE DELTA 15 DESATURASE.
GN DESB
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M.,
MURATA N.;
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in
altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSHIMA M., SUGIURA M., SASAKOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL; D13780; G600598; -.
DR EMBL; D90913; G1653388; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;
Query Match 4.0%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.76e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 114 ILVYHGWIRSHRTH 129
146 ILVYHGWIRSHRTH 161
RESULT 13
ID 007872 PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty
acid desaturase genes in the cyanobacterium Synechococcus sp. strain
PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL; U36389; G2197199; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;
Query Match 2.7%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.41e-08;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 74 ACGTMEWALFV 84
108 ACGTMEWALFV 118
RESULT 14
ID 074645 PRELIMINARY; PRT; 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEAE.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=F15;
RC MEDLINE; 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the trichothecene 3-O-acetyltransferase gene.
Analysis of the region around Trl101 and characterization of its
homologue from Fusarium sporotrichioides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1
FT NON_TER 193
SQ SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;
Query Match 2.0%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 6.19e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 186 HVHHLFP 193
324 HVHHLFP 331
RESULT 15
ID 044316 PRELIMINARY; PRT; 598 AA.
AC 044316;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE MALTOLOGOSYL TREHALOSE TREHALOHYDROLASE.
GN TRZ.
OS ARTHROBACTER SP.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIAE;
OC ACTINOMYCETES; MICROCOCCINAE; MICROCOCCACEAE; ARTHROBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Q36;
RX MEDLINE; 96195835.
RA MARUTA K., HATORI K., NAKADA T., KUBOTA M., SUGIMOTO T., KURIMOTO M.;
RT "Cloning and sequencing of trehalose biosynthesis genes from
Arthrobacter sp. Q36.";

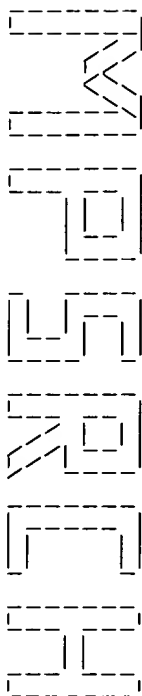
RL BIOCHIM. BIOPHYS. ACTA 1289:10-13(1996).
 DR EMBL; D63343; D1010313; -;
 DR PFAM; PF00128; alpha-amylase; 1.
 KW HYDROLASE.

SQ SEQUENCE 598 AA; 65832 MW; 22719107 CRC32;
 Query Match 2.0%; Score 8; DB 2; Length 598;
 Best Local Similarity 100.0%; Pred. No. 6.19e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 EAKKPVLG 15
 OY 343 EAKKPVLG 350

Search completed: Sat Aug 21 12:34:52 1999
 Job time : 91 secs.

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(TM)

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MSearch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:29:12 1999; MasPar time 15.63 Seconds

Tabular output not generated. 549,751 Million cell updates/sec

Title: 2US-09-219-935-9

Description: (1-404) from US09219935.pep

Sequence: 1 KFKRQSPSPFRFLNSRWMA.....DVTYEDPNLYGEIKVTAE 404

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a:geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.916; Variance 0.702; scale 4.153

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------------------|
| 1 | 404 | 100.0 | 404 | 7 | R37594 | Sequence of plastid d |
| 2 | 378 | 93.6 | 378 | 7 | R37591 | Sequence of microsome |
| 3 | 103 | 25.5 | 446 | 11 | R60499 | Linoleic-acid-desatur |
| 4 | 103 | 25.5 | 446 | 7 | R37593 | Sequence of a plastid |
| 5 | 43 | 10.6 | 435 | 11 | R60500 | Linoleic-acid-desatur |
| 6 | 36 | 8.9 | 447 | 24 | W13381 | Sesame omega-3 alipha |
| 7 | 36 | 8.9 | 453 | 7 | R37596 | Sequence of soybean p |
| 8 | 30 | 7.4 | 156 | 7 | R37598 | Sequence of a plastid |
| 9 | 28 | 6.9 | 383 | 11 | R60498 | Linoleic-acid-desatur |
| 10 | 28 | 6.9 | 386 | 7 | R37592 | Sequence of delta-15 |
| 11 | 27 | 6.7 | 380 | 7 | R37595 | Sequence of microsome |
| 12 | 9 | 2.2 | 126 | 7 | R37597 | Sequence of an intern |
| 13 | 9 | 2.2 | 387 | 10 | R53700 | Sequence of corn micr |
| 14 | 8 | 2.0 | 20 | 14 | R80284 | Trehalose releasing e |
| 15 | 8 | 2.0 | 597 | 14 | R80290 | Trehalose releasing e |
| 16 | 8 | 2.0 | 598 | 14 | R77471 | Trehalose releasing e |

| | | | | | | | |
|----|---|-----|------|----|--------|-----------------------|----------|
| 17 | 7 | 1.7 | 18 | 17 | R88585 | Spider venom calcium | 2.21e+01 |
| 18 | 7 | 1.7 | 18 | 2 | R07633 | N-terminal of Fractio | 2.21e+01 |
| 19 | 7 | 1.7 | 18 | 8 | R38424 | A-perla venom fracti | 2.21e+01 |
| 20 | 7 | 1.7 | 236 | 26 | W37715 | C. glutamicum Lys E p | 2.21e+01 |
| 21 | 7 | 1.7 | 289 | 19 | W01128 | Coat protein (short v | 2.21e+01 |
| 22 | 7 | 1.7 | 367 | 19 | R98899 | Coat protein (long v | 2.21e+01 |
| 23 | 7 | 1.7 | 367 | 34 | W61492 | Human fetuin glycopro | 2.21e+01 |
| 24 | 7 | 1.7 | 663 | 4 | R24101 | Marek's disease virus | 2.21e+01 |
| 25 | 6 | 1.5 | 202 | 39 | W67822 | Human secreted protei | 2.77e+02 |
| 26 | 6 | 1.5 | 203 | 39 | W67898 | Human secreted protei | 2.77e+02 |
| 27 | 6 | 1.5 | 214 | 2 | R10281 | Smilian immunodefici | 2.77e+02 |
| 28 | 6 | 1.5 | 239 | 36 | W80690 | S. pneumoniae protein | 2.77e+02 |
| 29 | 6 | 1.5 | 424 | 39 | W86150 | Human growth-related | 2.77e+02 |
| 30 | 6 | 1.5 | 424 | 36 | W79959 | Campylobacter jejuni | 2.77e+02 |
| 31 | 6 | 1.5 | 438 | 39 | W95500 | B. subtilis YabE rela | 2.77e+02 |
| 32 | 6 | 1.5 | 493 | 39 | W84068 | Human mitofusin Fzo h | 2.77e+02 |
| 33 | 6 | 1.5 | 519 | 39 | W89782 | Staphylococcus aureus | 2.77e+02 |
| 34 | 6 | 1.5 | 539 | 22 | W17973 | Coprinus cinereus lcc | 2.77e+02 |
| 35 | 6 | 1.5 | 543 | 30 | W37053 | S. putrefaciens EPO b | 2.77e+02 |
| 36 | 6 | 1.5 | 549 | 38 | W70898 | Acetyl-coenzyme A tra | 2.77e+02 |
| 37 | 6 | 1.5 | 707 | 38 | W83395 | Rabbit protein-couple | 2.77e+02 |
| 38 | 6 | 1.5 | 708 | 38 | W83395 | Human protein-couple | 2.77e+02 |
| 39 | 6 | 1.5 | 1012 | 39 | W95395 | IBDV VP2-VP3-VP4 poly | 2.77e+02 |
| 40 | 6 | 1.5 | 1978 | 35 | W69361 | Tetradotoxin-sensitiv | 2.77e+02 |
| 41 | 6 | 1.5 | 1988 | 35 | W69362 | Tetradotoxin-sensitiv | 2.77e+02 |
| 42 | 6 | 1.5 | 2100 | 39 | W89579 | Calcium permeable vol | 2.77e+02 |
| 43 | 6 | 1.5 | 2104 | 39 | W89578 | Calcium permeable vol | 2.77e+02 |
| 44 | 6 | 1.5 | 2105 | 39 | W89577 | Calcium permeable vol | 2.77e+02 |
| 45 | 6 | 1.5 | 2132 | 23 | W21739 | Variant rat DRG (SNS- | 2.77e+02 |

ALIGNMENTS

| | | | |
|-----------------------|--|---------------------------|----------------------------|
| RESULT 1 | ID | R37594 | standard; Protein: 404 AA. |
| AC | R37594; | 01-OCT-1993 (first entry) | |
| DE | Sequence of plastid delta-15 glycerolipid desaturase. | | |
| KW | Lipid composition; modification; fatty acid desaturase; enzyme. | | |
| OS | Brassica napus; clone pBNSFd-2. | | |
| PN | W09311245-A. | | |
| PD | 10-JUN-1993. | | |
| PF | 03-DEC-1992; U10284. | | |
| PR | 04-DEC-1991; US-804259. | | |
| PA | (DUPD) DU POINT DE NEMOURS & CO E. I. | | |
| PI | Browse J; Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, | | |
| PI | Yadav NS; | | |
| DR | WPI: 93-197063/24. | | |
| DR | N-PSDB; Q43206. | | |
| PT | Isolated nucleic acid fragment, for plant lipid compn. | | |
| PT | modification - comprises nucleic acid sequence encoding fatty | | |
| PT | acid desaturase or related enzyme with high aminoacid identity to | | |
| PT | specific polypeptide | | |
| PS | Disclosure; Page 140-141; 167pp; English. | | |
| CC | PCF3 was isolated from a cDNA library using a 5.2 kb Hind III | | |
| CC | fragment containing wild-type genomic DNA as a radiolabeled | | |
| CC | hybridization probe. One of the sequencing primers made to the PCF3 | | |
| CC | insert was also used. The identity of the expression product of PCF3 | | |
| CC | as the Arabidopsis microsomal delta-15 desaturase was confirmed by | | |
| CC | its biological overexpression in plant tissues. Conserved regions of | | |
| CC | R37592 are useful in designing long oligomers for hybridization as | | |
| CC | well as shorter ones for use as primers in the PCR. The sequences | | |
| CC | of useful regions are given in Q43213-Q43224. The cDNA inserts | | |
| CC | from PCF3 and PCW2 were used to isolate pBNSFd-3. Plasmid pBNSFd-3 | | |
| CC | was deposited as ATCC No. 68854. pBNSFd-3 (Q43206) corresp. to a | | |
| CC | novel Brassica napus seed desaturase different from that shown in | | |
| CC | Q43205. | | |
| SO | Sequence 404 AA: | | |
| Query Match | 100.0%; | Score 404; | DB 7; Length 404; |
| Best local Similarity | 100.0%; | Pred. 0.00e+00; | |
| Matches | 404; Conservative | 0; Mismatches | 0; Indels 0; Gaps 0; |

Db 1 fkrfgssprflnsnvalnvtrptvdsassprleeeptktrfdgppppfnladir 60
| | | | |
QY 1 fkrfgssssprflnsnvalnvtrptvdsassprleeeptktrfdgppppfnladir 60
Db 61 aatlpkhwknwpkmsyvvrelaivafalaagaaylmmwlpwlylaagtmfvalfvlg 120
| | | | |
QY 61 aatlpkhwknwpkmsyvvrelaivafalaagaaylmmwlpwlylaagtmfvalfvlg 120
Db 121 hdcghgsfndprlmsvvgllhssllvpyhgwrisrthqnqghvendeswhpmsek1 180
| | | | |
QY 121 hdcghgsfndprlmsvvgllhssllvpyhgwrisrthqnqghvendeswhpmsek1 180
Db 181 ykxldkpttrfftrfplwmlayprfylvarepgksgshyhpdsdlflpkerndvltstacw 240
| | | | |
QY 181 ykxldkpttrfftrfplwmlayprfylvarepgksgshyhpdsdlflpkerndvltstacw 240
Db 241 tamavllvclnfvmgpmqmklyvipywlmwmdfctytlhhbhedk1pwysgkewsy1 300
| | | | |
QY 241 tamavllvclnfvmgpmqmklyvipywlmwmdfctytlhhbhedk1pwysgkewsy1 300
Db 301 rrglctldrdyglmmhhdigtvhlhlfpg4lphynlveateaakpvl9kyyrepdksg 360
| | | | |
QY 301 rrglctldrdyglmmhhdigtvhlhlfpg4lphynlveateaakpvl9kyyrepdksg 360
Db 361 plrphllglakskedhfvsgdegvvyvyeadpnllygeikvtae 404
| | | | |
QY 361 plrphllglakskedhfvsgdegvvyvyeadpnllygeikvtae 404

RESULT 2

ID R37591 standard; Protein: 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone pBNSF3-f2.
PN M09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPT; 93-197063/24.
DR N-PSDB; Q43205.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 136-138; 167pp; English.
PC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate pBNSF3-2, plasmid pBNSF3-2
CC was deposited as ATCC No. 68854. pBNSF3-3 (Q43205) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA;

Query Match 93.6%; Score 378; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 378; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D 1 ltydssssppleeeptktrfdgppppfnladiraaatlpkhwknwpkmsyvvrelaiv 60
| | | | |
QY 27 ltydssssppleeeptktrfdgppppfnladiraaatlpkhwknwpkmsyvvrelaiv 86

D 61 falaagaaylmmwlpwlyviaggtmfvalfvlgchcghgsfndprlmsvvgllhss1 120
| | | | |
QY 87 falaagaaylmmwlpwlyviaggtmfvalfvlgchcghgsfndprlmsvvgllhss1 146
Db 121 lpyhgwrisrthqnqghvendeswhpmsek1yxsldkpttrfftrfplwmlayprfvl 180
| | | | |
QY 147 lpyhgwrisrthqnqghvendeswhpmsek1yxsldkpttrfftrfplwmlayprfvl 206
Db 181 warspgksgshyhpdsdlflpkerndvltstacwtamavllvclnfvmgpmqmklyv1p 240
| | | | |
QY 207 warspgksgshyhpdsdlflpkerndvltstacwtamavllvclnfvmgpmqmklyv1p 266
Db 241 ywlmwmdfctytlhhbhedk1pwysgkewsy1rgglctldrdyglmmhhdigtvhl 300
| | | | |
QY 267 ywlmwmdfctytlhhbhedk1pwysgkewsy1rgglctldrdyglmmhhdigtvhl 326
Db 301 hhlfpq4lphynlveateaakpvl9kyyrepdksgp1p1hllglakskedhfvsgdegdv 360
| | | | |
QY 327 hhlfpq4lphynlveateaakpvl9kyyrepdksgp1p1hllglakskedhfvsgdegdv 386
Db 361 vvyeadpnllygeikvtae 378
| | | | |
QY 387 vvyeadpnllygeikvtae 404

RESULT 3

ID R60499 standard; Protein: 446 AA.
AC R60499;
DT 28-MAR-1995 (first entry)
DE linoleic-acid-desaturase fadd.
KW linoleic-acid-desaturase; fadd; transgenic plant; crop improvement;
KW linoleic acid.
OS Arabidopsis.
PN M09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Aronold VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
PI WPT; 94-279758/34.
DR N-PSDB; Q71210.
PT Genetically transformed plants with altered linolenic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 75-77; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of linoleic-
CC acid-desaturase fadd of Arabidopsis are provided.
SQ Sequence 446 AA;

Query Match 25.5%; Score 103; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.37e-160;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

D 307 lpywlmwmdfctytlhhbhedk1pwysgkewsy1rgglctldrdyglmmhhdigtvhl 366
| | | | |
QY 265 lpywlmwmdfctytlhhbhedk1pwysgkewsy1rgglctldrdyglmmhhdigtvhl 324
Db 367 vlnhllfpq4lphynlveateaakpvl9kyyrepdksgp1p1hll 409
| | | | |
QY 325 vlnhllfpq4lphynlveateaakpvl9kyyrepdksgp1p1hll 367

RESULT 4

ID R37593 standard; Protein: 446 AA.
AC R37593;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN M09311245-A.

PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 132-134; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show and overall homology of approx.
CC 80%.

SO Sequence 446 AA;

Query Match 25.58; Score 103; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 9,37e-160;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 307 lpywtvwmwldfttylhbhbkelpwrgkewylrglttdrgylnnhhdgth 366
|||||
QY 265 lptwimwldfttylhbhbkelpwrgkewylrglttdrgylnnhhdgth 324
|||||

DB 367 vlhhlfqdlphylveateakpvlqkyrepeksdp1p1h1 409
|||||
QY 325 vlhhlfqdlphylveateakpvlqkyrepeksdp1p1h1 367
|||||

RESULT 5
ID R60500 standard; Protein: 435 AA.
AC R60500;
DT 28-MAR-1995 (first entry)
DE linoletic-acid-desaturase fadE.
KW linoletic-acid-desaturase; fadE; transgenic plant; crop improvement;
KM linoletic acid.
OS Arabidopsis.
PN MO9418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Aronold VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: Q71211.
PT Genetically transformed plants with altered linoletic acid
PT content - cont recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144pp; English.
CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fadE of Arabidopsis are provided.
CC Sequence 435 AA;

Query Match 10.68; Score 43; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 9,36e-56;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 349 lnnhhdgthv1h1lfpqdlphylveateakpvlqkyre 391
|||||
QY 314 lnnhhdgthv1h1lfpqdlphylveateakpvlqkyre 356
|||||

RESULT 6
ID W13381 standard; Protein: 447 AA.
AC W13381;
DT 02-DEC-1997 (first entry)
DE Sesame omega-3 aliphatic acid desaturase.
KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
KW linoletic acid; recombinant production.
OS Sesamum indicum.
PN J09065882-A.
PD 11-MAR-1997.
PE 01-SEP-1995; 225145.
PR (TOYA-) TOYAMA KEN.
PA WPI: 97-220417/20.
DR N-PSDB: T62066.
PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
PT engineering to modify fats and oils in agricultural products
PS Claim 6; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
CC sequence can be used in genetic engineering to modify fats and oils in
CC agricultural products. The gene or enzyme can be introduced into a plant
CC to modify the aliphatic acid composition in its oils and fats, to give
CC oils and fats with a high content of linoletic acid. Antisense DNA can
CC be introduced into a plant to inhibit the expression of the gene, so
CC that oils and fats with little or no linoletic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.

SO Sequence 447 AA;

Query Match 8.98; Score 36; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 5,93e-44;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 323 vtylhbhghedkelpwrgkewylrglttdrgy 358
|||||
QY 277 vtylhbhghedkelpwrgkewylrglttdrgy 312
|||||

RESULT 7
ID R37596 standard; Protein: 453 AA.
AC R37596;
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS glycine max. clone pSPD-118bwp.
PN MO9311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43208.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 148-150; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15

CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
CC deposited under ATCC 68874. Soybean microsomal delta-15
CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC encoding related desaturases from soybean. The insert of
CC pSFD-118bp contained a stretch of 1675 nucleotides which contained
CC an open-reading frame encoding a polypeptide (R37596) of about
CC 80% identity with, and colinear with, the Arabidopsis plastid
CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC to 382 encode the putative plastid transit peptide, colinear with
CC and sharing some homology with the transit peptide described for
CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ Sequence 453 AA;

Query Match 8.9%; Score 36; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 5.93e-44;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 327 vtlyhhghedklpwyrgkwsyirglttldrdyg 362
|||||
Qy 277 VTYLHHGHEDKLPWYRGKWSYIRGLTTLDRDYG 312

RESULT 8
ID R37598 standard; Protein; 156 AA.
AC R37598;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pFadX-2 and pYacp7.
PN M09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pFadX-2 and
CC pYacp7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 7.4%; Score 30; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 5.28e-34;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 95 aggtmfwtlvtghdchgsfndprlnsv 124
|||||
Qy 108 AOGTFMALFVLGHDCGHSFNDPRLNSV 137

RESULT 9
ID R60498 standard; Protein; 383 AA.
AC R60498;
DT 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase; fad3.
KW transgenic plant; crop improvement; yeast artificial chromosome;

KW YAC; linoleic acid.
OS Brassica napus.
PN M09418337-A.
PD 18-AUG-1994.
PE 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Aronold VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: Q71203
PT Genetically transformed plants with altered linoleic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 69-71; 144pp; English.
CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
CC isolated from a YAC library using RFLP 220 and ASA2 markers as
CC probes. Isolated DNA was amplified using the primers given in
CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
CC identified in YAC EW7D11.
SQ Sequence 383 AA;

Query Match 6.9%; Score 28; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.00e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 123 llvpybwtshrtbqnbhgvndesw 150
|||||
Qy 146 ILVPHYGWRISHTRHONHGVNDESW 173

RESULT 10
ID R37592 standard; Protein; 386 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pCF3.
PN M09311245-A.
PD 10-JUN-1993.
PE 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: Q43202.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 127-129; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224.
SQ Sequence 386 AA;

Query Match 6.9%; Score 28; DB 7; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.00e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dh 126 llvpybwtshrtbqnbhgvndesw 153
|||||
Qy 146 ILVPHYGWRISHTRHONHGVNDESW 173

RESULT 11
ID R37592 standard; Protein: 380 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pXFL.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992: U10284.
PI 04-DEC-1991: US-804259.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadau NS;
DR N-PSDB: 043207.
DR N-PSDB: 043207.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PS Disclosure: Page 144-146: 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCF3 insert was also used. The identity of the expression product of PCF3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by CC its biological overexpression in plant tissues. Conserved regions of CC R37592 are useful in designing long oligomers for hybridization as well as shorter ones for use as primers in the PCR. The sequences CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15 CC desaturase cDNA was used as a hybridization probe to isolate a CC glycerolipid desaturase cDNA from soybean. Plasmid pXFL was CC deposited under ATCC 68874.
SQ Sequence 380 AA;

Query Match 6.7%; Score 27; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 4.27e-29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 295 nihndictvnhlfqthphylveat 321
|||
QY 316 NIHHDIGTHVHLEPQIPHYHLEAT 342

RESULT 12
ID R37597 standard; Protein: 126 AA.
AC R37597;
DT 01-OCT-1993 (first entry)
DE Sequence of an internal region of a corn seed delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Zea mays, clone pPCR20.
PN W09311245-A.
PD 10-JUN-1993.
PR 03-DEC-1992: U10284.
PR 04-DEC-1991: US-804259.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM, Yadau NS;
DR N-PSDB: 043209.
DR N-PSDB: 043209.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty acid desaturase or related enzyme with high aminoacid identity to specific polypeptide
PS Disclosure: Page 152-153: 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III fragment containing wild-type genomic DNA as a radiolabeled hybridization probe. One of the sequencing primers made to the PCF3 insert was also used. The identity of the expression product of PCF3 as the Arabidopsis microsomal delta-15 desaturase was confirmed by CC its biological overexpression in plant tissues. Conserved regions of

CC R37592 are useful in designing long oligomers for hybridization as CC well as shorter ones for use as primers in the PCR. The sequences CC of useful regions are given in Q43213-Q43224. Q43209 is the CC complete nucleotide sequence of a 396 bp polymerase chain reaction CC product derived from corn seed mRNA that is found in the insert of CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to CC the amplification primers described in Q43211 and Q43212 CC respectively. Nucleotides 31 to 363 encode a region that is 61.9% CC identical to the region between amino acids 137 and 249 of R37591.
SQ Sequence 126 AA;

Query Match 2.2%; Score 9; DB 7; Length 126;
Best Local Similarity 100.0%; Pred. No. 7.93e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 118 vtylhhgh 126
|||
QY 277 VTYLHHGH 285

RESULT 13
ID R53700 standard; Protein: 387 AA.
AC R53700;
DT 09-NOV-1994 (first entry)
DE Sequence of corn microsomal delta-12 desaturase deduced from the DE cDNA in plasmid pRad2 1.
KW Fatty acid; desaturase; lipid; unsaturated; transgenic plant.
OS Zea mays.
PN W09411516-A.
PD 26-MAY-1994.
PR 15-OCT-1993: U09987.
PR 17-NOV-1992: US-977339.
PI (DUPO) DU PONT DE NEMOURS & CO E.I.
PI Lightner JE, Okuley J;
DR WPI: 94-183515/22.
DR N-PSDB: Q66071.
PT Genes for fatty acid desaturase enzymes - permit alteration of PT plant lipid composition
PS Claim 13: Page 124-126: 147pp; English.
CC Corn microsomal delta-12 desaturase cDNA was isolated using a PCR CC approach. A cDNA library was made to poly A+ mRNA from developing CC corn embryos. This library was used as template for PCR using sets CC of degenerate oligos NS3 (Q66075) and RB5A/B (Q66077, Q66078) as CC sense and antisense primers, respectively. NS3 and RB5A/B corresp. CC to stretches of AAs 101-109 and 318-326, respectively, of R53697, CC which are conserved in most microsomal delta-12 desaturases. A PCR CC product of 720bp was purified and used as a probe for screening the CC corn cDNA library. A plaque was purified and found to encode CC microsomal delta-12 desaturase truncated at the 3' end. This cDNA CC was used to probe the corn cDNA library again. The clone congt. CC the longest insert, designated pRad2 1 was sequenced completely CC (Q66071). An isolated nucleic acid fragment
CC wherein the nucleic acid identity is 90% or greater to CC encoding fatty acid desaturases and related enzymes is claimed CC 066071 is claimed. A method to isolate nucleic acid fragments CC which comprises: comparing AA sequences in R53697-R53702 and other CC fatty acid desaturase sequences; identifying conserved sequences of CC 4 or more AAs; designed degenerate oligos based on the conserved CC sequences; and using the oligos to isolated sequences encoding fatty CC acid desaturases and desaturase-related enzymes.
SQ Sequence 387 AA;

Query Match 2.2%; Score 9; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 7.93e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 92 wplywiag 100
|||
QY 102 WPLYWIAG 110

RESULT 14
ID R80294 standard; Protein: 20 AA.

AC R80294: 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme N-terminal fragment.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetraosyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Arthrobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
from a non-reducing saccharide having a trehalose structure as an
end unit.
PS Example 4: Page 25: 45pp: English.
CC The trehalose releasing enzyme can be used for the preparation of
CC trehalose with high yields and efficiency from non-reducing
CC saccharides such as alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetraosyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
CC This is the N-terminal sequence of the enzyme.
SQ Sequence 20 AA;

Query Match 2.0%; Score 8; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.43e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 eaakpylg 14
|||
OY 343 EAAKPYLG 350

RESULT 15
ID R80290 standard: Protein; 597 AA.
AC R80290:
DT 19-JAN-1996 (first entry)
DE Trehalose releasing enzyme.
KW Enzyme; trehalose; alpha-glucosyltrehalose; alpha-maltosyltrehalose;
KW alpha-maltotriosyltrehalose; alpha-maltotetraosyltrehalose;
KW maltopentaosyltrehalose; sweetener; taste-improving agent;
KW stabiliser; filler; excipient; adjuvant; foodstuffs; cosmetics;
KW pharmaceuticals.
OS Arthrobacter sp. Q36.
PN EP-671470-A2.
PD 13-SEP-1995.
PE 07-MAR-1995: 301474.
PR 07-MAR-1994: JP-059840.
PR 07-MAR-1994: JP-059834.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hattori K, Kubota M, Sugimoto T, Tsusaki K;
DR WPI: 95-312772/41.
DR N-PSDB: Q98670.
PT DNA encoding a trehalose releasing enzyme - which releases trehalose
from a non-reducing saccharide having a trehalose structure as an
end unit.
PS Claim 3: Page 24-25: 45pp: English.
CC This enzyme can be used for the preparation of trehalose with high
CC yields and efficiency from non-reducing saccharides such as
CC alpha-glucosyltrehalose, alpha-maltosyltrehalose,
CC alpha-maltotriosyltrehalose, alpha-maltotetraosyltrehalose and
CC maltopentaosyltrehalose. The trehalose can be used as a sweetener,
CC taste-improving agent, quality-improving agent, stabiliser, filler,
CC excipient or adjuvant in food products cosmetics and pharmaceuticals.
SQ Sequence 597 AA;

Query Match 2.0%; Score 8; DB 14; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.43e+00;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 7 eaakpylg 14
|||
OY 343 EAAKPYLG 350

Search completed: Sat Aug 21 12:31:07 1999
Job time : 115 secs.

MIRISIRI (TM)

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MSPRCH_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:35:11 1999; MasPar time 5.41 Seconds

Tabular output not generated. 758.169 Million cell updates/sec

Title: >US-09-219-935-9

Description: (1-404) from US09219935.pep

Perfect Score: 404

Sequence: 1 FKFRQSPSPFRRLNSRWMA.....DVYYEADPNLXGEIKVTAE 404

Scoring table: TABLE uniprottable

Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: a-issued

1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 2.765; Variance 0.703; scale 3.933

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 404 | 100.0 | 404 | 3 | PCT-US92-1 Sequence 9, Applicatio | 0.00e+00 |
| 2 | 378 | 93.6 | 378 | 3 | PCT-US92-1 Sequence 7, Applicatio | 0.00e+00 |
| 3 | 103 | 25.5 | 446 | 3 | PCT-US94-0 Sequence 10, Applicati | 2.60e-152 |
| 4 | 103 | 25.5 | 446 | 3 | PCT-US92-1 Sequence 5, Applicatio | 2.60e-152 |
| 5 | 43 | 10.6 | 435 | 3 | PCT-US94-0 Sequence 12, Applicati | 1.49e-53 |
| 6 | 36 | 8.9 | 453 | 3 | PCT-US92-1 Sequence 13, Applicati | 2.37e-42 |
| 7 | 31 | 7.7 | 156 | 3 | PCT-US92-1 Sequence 17, Applicati | 1.90e-34 |
| 8 | 28 | 6.9 | 383 | 3 | PCT-US94-0 Sequence 2, Applicatio | 9.34e-30 |
| 9 | 28 | 6.9 | 386 | 3 | PCT-US92-1 Sequence 2, Applicatio | 9.34e-30 |
| 10 | 27 | 6.7 | 380 | 3 | PCT-US92-1 Sequence 11, Applicati | 3.34e-28 |
| 11 | 25 | 6.2 | 372 | 2 | US-08-320- Sequence 6, Applicatio | 4.11e-25 |
| 12 | 25 | 6.2 | 372 | 2 | US-08-320- Sequence 22, Applicati | 4.11e-25 |
| 13 | 25 | 6.2 | 372 | 1 | US-08-314- Sequence 6, Applicatio | 4.11e-25 |
| 14 | 25 | 6.2 | 372 | 1 | US-08-314- Sequence 22, Applicati | 4.11e-25 |
| 15 | 22 | 5.4 | 371 | 1 | US-08-314- Sequence 16, Applicati | 1.57e-20 |
| 16 | 22 | 5.4 | 371 | 1 | US-08-314- Sequence 12, Applicati | 1.57e-20 |
| 17 | 22 | 5.4 | 372 | 2 | US-08-320- Sequence 16, Applicati | 1.57e-20 |
| 18 | 22 | 5.4 | 372 | 2 | US-08-320- Sequence 12, Applicati | 1.57e-20 |
| 19 | 18 | 4.5 | 402 | 2 | US-08-320- Sequence 10, Applicati | 1.52e-14 |
| 20 | 18 | 4.5 | 402 | 2 | US-08-320- Sequence 18, Applicati | 1.52e-14 |
| 21 | 18 | 4.5 | 401 | 1 | US-08-314- Sequence 10, Applicati | 1.52e-14 |
| 22 | 18 | 4.5 | 401 | 1 | US-08-314- Sequence 18, Applicati | 1.52e-14 |
| 23 | 12 | 3.0 | 37 | 1 | US-08-314- Sequence 26, Applicati | 5.32e-06 |

| | | | | | | |
|----|----|-----|-----|---|-----------------------------------|----------|
| 24 | 12 | 3.0 | 37 | 1 | US-08-314- Sequence 8, Applicatio | 5.32e-06 |
| 25 | 12 | 3.0 | 37 | 2 | US-08-320- Sequence 8, Applicatio | 5.32e-06 |
| 26 | 12 | 3.0 | 37 | 2 | US-08-320- Sequence 26, Applicati | 5.32e-06 |
| 27 | 11 | 2.7 | 40 | 2 | US-08-320- Sequence 24, Applicati | 1.18e-04 |
| 28 | 11 | 2.7 | 40 | 2 | US-08-320- Sequence 4, Applicatio | 1.18e-04 |
| 29 | 11 | 2.7 | 40 | 1 | US-08-314- Sequence 4, Applicatio | 1.18e-04 |
| 30 | 11 | 2.7 | 40 | 1 | US-08-314- Sequence 24, Applicati | 1.18e-04 |
| 31 | 9 | 2.2 | 9 | 3 | PCT-US94-0 Sequence 56, Applicati | 4.50e-02 |
| 32 | 9 | 2.2 | 126 | 3 | PCT-US92-1 Sequence 15, Applicati | 4.50e-02 |
| 33 | 8 | 2.0 | 8 | 2 | US-08-789- Sequence 8, Applicatio | 7.51e-01 |
| 34 | 8 | 2.0 | 8 | 3 | PCT-US94-0 Sequence 70, Applicati | 7.51e-01 |
| 35 | 8 | 2.0 | 8 | 3 | PCT-US94-0 Sequence 63, Applicati | 7.51e-01 |
| 36 | 8 | 2.0 | 20 | 1 | US-08-607- Sequence 6, Applicatio | 7.51e-01 |
| 37 | 8 | 2.0 | 20 | 1 | US-08-399- Sequence 6, Applicatio | 7.51e-01 |
| 38 | 8 | 2.0 | 20 | 2 | US-08-605- Sequence 6, Applicatio | 7.51e-01 |
| 39 | 8 | 2.0 | 597 | 1 | US-08-607- Sequence 4, Applicatio | 7.51e-01 |
| 40 | 8 | 2.0 | 597 | 2 | US-08-961- Sequence 4, Applicatio | 7.51e-01 |
| 41 | 8 | 2.0 | 597 | 2 | US-08-605- Sequence 4, Applicatio | 7.51e-01 |
| 42 | 8 | 2.0 | 598 | 1 | US-08-607- Sequence 14, Applicati | 7.51e-01 |
| 43 | 8 | 2.0 | 598 | 2 | US-08-399- Sequence 14, Applicati | 7.51e-01 |
| 44 | 8 | 2.0 | 598 | 2 | US-08-605- Sequence 14, Applicati | 7.51e-01 |
| 45 | 8 | 2.0 | 598 | 2 | US-08-961- Sequence 14, Applicati | 7.51e-01 |

ALIGNMENTS

RESULT 1
ID PCT-US92-10284-9 STANDARD: PRT: 404 AA.

AC xxxxxx

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Sequence 9, Application PC/TUS9210284

GENERAL INFORMATION:

APPLICANT: Browne, John, Kinney, Anthony J.,

APPLICANT: Yadav, Narendra S., Perez-Grau, Luis

TITLE OF INVENTION: Fatty Acid Desaturase Genes

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STATE: Delaware

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10284

FILING DATE: 19921203

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/804,259

FILING DATE: 4 DECEMBER 1991

ATTORNEY/AGENT INFORMATION:

NAME: Floyd, Linda A.

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1036-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEX: 835420

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 404 amino acids

CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;

Query Match 25.5%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,606-152;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 366
|||
QY 265 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 324
|||
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPHLL 409
|||
QY 325 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPHLL 367
|||

RESULT 4
ID PCT-US92-10284-5 STANDARD; PRT: 446 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 5, Application PC/TUS9210284
XX
CC Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;

Query Match 25.5%; Score 103; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,606-152;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 307 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 366
|||
QY 265 IPWINVMWLDFTYLLHHGHEDKLPWYRGKEMSYLRGGLTTLDRDYGILNNHHIDIGTH 324
|||
Db 367 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPHLL 409
|||
QY 325 VIHHLFPOIPHYHLVEATEAKPVLGKYYRPPDKSGPLPHLL 367
|||

RESULT 5
ID PCT-US94-01321-12 STANDARD; PRT: 435 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 12, Application PC/TUS9401321
XX
CC Sequence 12, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 435 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 435 AA; 50136 MW; 1054240 CN;

Query Match 10.6%; Score 43; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,496-53;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 349 INNHHIDIGTHVIHHLFPOIPHYHLVEATEAKPVLGKYYREP 391
|||
QY 314 INNHHIDIGTHVIHHLFPOIPHYHLVEATEAKPVLGKYYREP 356
|||

RESULT 6
ID PCT-US92-10284-13 STANDARD; PRT: 453 AA.
XX
AC xxxxxx
XX
DT

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DE      Sequence 13, Application PC/TUS9210284
XX
CC
CC      Sequence 13, Application PC/TUS9210284
CC      GENERAL INFORMATION:
CC      APPLICANT: Browsee, John, Kinney, Anthony J.,
CC      APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC      APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC      TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC      TITLE OF INVENTION: from Plants
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: E. I. du Pont de Nemours and Company
CC      STREET: 1007 Market Street
CC      CITY: Wilmington
CC      STATE: Delaware
CC      COUNTRY: U.S.A.
CC      ZIP: 19898
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: Macintosh
CC      OPERATING SYSTEM: Macintosh System, 6.0
CC      SOFTWARE: Microsoft Word, 4.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US92/10284
CC      FILING DATE: 19921203
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/804,259
CC      FILING DATE: 4 DECEMBER 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Floyd, Linda A.
CC      REGISTRATION NUMBER: 33,692
CC      REFERENCE/DOCKET NUMBER: BB-1036-A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 13:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 453 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 453 AA; 51362 MM; 1146882 CN;
SQ
Query Match          8.9%; Score 36; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.37e-42;
Matches    36; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
Db      327 VTYLHHGHEDKLPYRGKEWSYLRLGGITTLDRDYG 362
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Oy      277 VTYLHHGHEDKLPYRGKEWSYLRLGGITTLDRDYG 312

RESULT 7
ID      PCT-US92-10284-17 STANDARD; PRT; 156 AA.
XX
AC      xxxxxx
DT
XX
Sequence 17, Application PC/TUS9210284
DE
CC      Sequence 17, Application PC/TUS9210284
CC      GENERAL INFORMATION:
CC      APPLICANT: Browsee, John, Kinney, Anthony J.,
CC      APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC      APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC      TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC      TITLE OF INVENTION: from Plants
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:

```

```

CC ADDRESS: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEetical: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pfdx-2 and pYacp7
CC SEQUENCE 156 AA; 17771 MW; 128823 CN;
SQ
Query Match 7.7%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 1,90e-34;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 GHLLSSILVYHGMRIHSHRTHHNGHVEN 156
QY 139 GHLLSSILVYHGMRIHSHRTHHNGHVEN 169
RESULT 8
ID PCT-US94-01321-2 STANDARD; PRT; 383 AA.
XX xxxxxx
XX
XX
XX Sequence 2, Application PC/TUS9401321
XX DE
XX Sequence 2, Application PC/TUS9401321
XX
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: In Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994

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RESULT 11
ID US-08-320-982-6 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 6, Application US/08320982
XX
CC Sequence 6, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ
Query Match 6.2%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTHVHHLFPOIPHYHLEAT 25
Y 318 HHDIGTHVHHLFPOIPHYHLEAT 342
|||||
RESULT 12
ID US-08-320-982-22 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 22, Application US/08320982
XX
CC Sequence 22, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4331 MW: 8403 CN;
SQ
Query Match 6.2%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTHVHHLFPOIPHYHLEAT 25
Y 318 HHDIGTHVHHLFPOIPHYHLEAT 342
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RESULT 13
ID US-08-314-596-6 STANDARD: PRT; 37 AA.
AC xxxxxx
XX
DT
XX Sequence 6, Application US/08314596
XX
CC Sequence 6, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;

Query Match 6.28; Score 25; DB 1; Length 37;
Best Local Similarity 100.08; Pred. No. 4,11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 25
QY 318 HHDIQTHVHHLFPQIPHYHLEAT 342

RESULT 14
ID US-08-314-596-22 STANDARD; PRT: 37 AA.
XX xxxxxx
AC
DT
XX
XX
DE Sequence 22, Application US/08314596
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: 48
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;

Query Match 6.28; Score 25; DB 1; Length 37;
Best Local Similarity 100.08; Pred. No. 4,11e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 25
QY 318 HHDIQTHVHHLFPQIPHYHLEAT 342

RESULT 15
ID US-08-314-596-16 STANDARD; PRT: 37 AA.
XX xxxxxx
AC
DT
XX
XX
DE Sequence 16, Application US/08314596
CC Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: 48
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DABRY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4407 MW; 7119 CN;

Query Match 5.48; Score 22; DB 1; Length 37;
Best Local Similarity 100.08; Pred. No. 1,57e-20;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIQTHVHHLFPQIPHYHLEAT 22

|||||
Oy 318 HHDICTHYIHHLFOIPIPHYLV 339

Search completed: Sat Aug 21 12:35:42 1999
Job time : 31 secs.


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Best Local Similarity 100.0%; Pred. No. 2.07e-58;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 179 VGHILHSSILVPGHGRISRTTHQNHGH 207
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OY 117 VGHILHSSILVPGHGRISRTTHQNHGH 145

RESULT 4
ENTRY #type complete
TITLE omega-3 fatty acid desaturase (PC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 19-Feb-1999
ACCESSION T01697
REFERENCE Z14400
AUTHORS Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
#journal Kusano, T.
#title Plant Mol. Biol. (1998) 36:297-306
#accession Two maize genes encoding omega-3 fatty acid desaturase and
T01697 their differential expression to temperature.
#status Preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-443 #label BER
#cross_references EMBL:D63954; NID:d1164453; PID:d1023306
#experimental_source strain honey bantum

GENETICS
#gene FAD7
#introns 163/2; 193/2; 215/3; 246/3; 308/3; 335/3; 381/3
KEYWORDS oxidoreductase
SUMMARY #length 443 #molecular_weight 49437 #checksum 8872

Query Match 7.6%; Score 29; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 2.07e-58;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 178 VGHILHSSILVPGHGRISRTTHQNHGH 206
|||||
OY 117 VGHILHSSILVPGHGRISRTTHQNHGH 145

RESULT 5
ENTRY #type complete
TITLE omega-3 fatty acid desaturase (PC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 17-Mar-1999
ACCESSION PQ0812
REFERENCE Y02335
AUTHORS Yadav, N.S.; Wierzbicki, A.; Aegeerter, M.; Caster, C.S.;
Percer-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browe, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross_references MIMD:94302147
#contents CDNA:BND
#accession PQ0812
#molecule_type mRNA
#residues 1-404 #label YAD
#cross_references GB:I22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
Plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular_weight 46617 #checksum 9400

Query Match 7.1%; Score 27; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.92e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 316 NIHHDIGTHVHHLFPOIPHYLVEAT 342
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QY 295 NIHHDIGTHVHHLFPOIPHYLVEAT 321

RESULT 6
ENTRY JQ2336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse-ear
cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS JQ2336: A49503
REFERENCE JQ2335
#authors Yadev, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession JQ2336
#molecule_type mRNA
#residues 1-446 #label YAD

REFERENCE A49503
#authors Iba, K.; Gibson, S.; Nishimura, T.; Fuse, T.; Nishimura, M.;
Arondel, V.; Hugly, S.; Somerville, C.
#journal J. Biol. Chem. (1993) 268:24099-24105
#title A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and
chloroplast copy number of the fat7 mutant of Arabidopsis
thaliana.
#cross-references MUID:94043239
#accession A49503
#status Preliminary
#molecule_type DNA
#residues 1-446 #label IBA
#cross-references GB:DI4007; NID:9461160; PID:d1003612; PID:g541653
#note Sequence extracted from NCBI backbone (NCBIN:139485,
NCBIP:139486)

COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
KEYWORDS #superfamily omega-3 fatty acid desaturase
oxidoreductase
SUMMARY #length 446 #molecular_weight 51174 #checksum 4653

Query Match 7.1%; Score 27; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.92e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 NIHHDIGTHVHHLFPOIPHYLVEAT 384
|||||
QY 295 NIHHDIGTHVHHLFPOIPHYLVEAT 321

RESULT 7
ENTRY JQ2339 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS JQ2339
REFERENCE JQ2335
#authors Yadev, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
#molecule_type mRNA
#residues 1-453 #label YAD

COMMENT #cross-references GB:L22965; NID:9408791; PID:g408792
This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
KEYWORDS #superfamily omega-3 fatty acid desaturase
chloroplast; oxidoreductase
SUMMARY #length 453 #molecular_weight 51362 #checksum 7549

Query Match 7.1%; Score 27; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.92e-52;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 366 NIHHDIGTHVHHLFPOIPHYLVEAT 392
|||||
QY 295 NIHHDIGTHVHHLFPOIPHYLVEAT 321

RESULT 8
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references MUID:95011632
#accession JC2555
#status Preliminary
#molecule_type mRNA
#residues 1-379 #label HAM
#cross-references DDBJ:D26509; NID:g1311480; PID:d1006059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
SUMMARY #length 379 #molecular_weight 44149 #checksum 1940

Query Match 6.6%; Score 25; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 1.53e-46;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 264 KLPYRKREWSYLRGLTYVDROYG 288
|||||
QY 267 KLPYRKREWSYLRGLTYVDROYG 291

RESULT 9
ENTRY JQ2337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS JQ2337
REFERENCE JQ2335
#authors Yadev, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BN3
#accession JQ2337
#molecule_type mRNA

##residues 1-377 ##label YAD
##cross-references GB:I22962; NID:g408491; PID:g408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43358 #checksum 3294

Query Match 6.3%; Score 24; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 287 NIHHDIGTHVHLEFPQIPHYHLV 310
|||
QY 295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 10
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES #formal name Brassica napus #common name rape
ORGANISM 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
DATE 20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman, H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227

##status preliminary: not compared with conceptual translation
##molecule_type nucleic acid
##residues 1-383 ##label ARO
##cross-references GB:I01418; NID:g167147; PID:g167148
#experimental_source developing seed
#note sequence extracted from NCBI backbone (NCBIF:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 6.3%; Score 24; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NIHHDIGTHVHLEFPQIPHYHLV 316
|||
QY 295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 11
ENTRY J02335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
ORGANISM #formal name Arabidopsis thaliana #common name mouse-ear
cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
12-Mar-1999
ACCESSIONS J02335
REFERENCE J02335 T02487
#authors Yadev, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02335
#molecule_type mRNA

##residues 1-386 ##label YAD
REFERENCE 214675
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23f1 genomic
sequence.
#accession T02487
#status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-386 ##label ROU
##cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.

GENETICS
#map_position II
#introns 103/2; 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#note F23f1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044

Query Match 6.3%; Score 24; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.28e-43;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 NIHHDIGTHVHLEFPQIPHYHLV 319
|||
QY 295 NIHHDIGTHVHLEFPQIPHYHLV 318

RESULT 12
ENTRY S52650 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - Synechocystis
sp. (strain PCC6803)
ALTERNATE_NAMES delta 15 desaturase
ORGANISM #formal name Synechocystis sp.
#variety
DATE 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change
17-Mar-1999
ACCESSIONS S52650; S75843
REFERENCE S52649
#authors Sakamoto, T.; Los, D.A.; Higashi, S.; Wada, H.; Nishida, I.;
Omorii, M.; Murata, N.
#journal Plant Mol. Biol. (1994) 26:249-263
#title Cloning of omega-3 desaturase from cyanobacteria and its use
in altering the degree of membrane-lipid unsaturation.
#cross-references MUID:95035996
#accession S52650
##molecule_type DNA
##residues 1-359 ##label SAK
##cross-references GB:D13780; NID:g600596; PID:d1003430; PID:g600598
#note the authors translated the initiation codon GTG for
residue 1 as Val

REFERENCE S74322
#authors Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.;
Nakamura, Y.; Miyajima, N.; Hirosewa, M.; Sugiyama, M.;
Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.;
Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpou,
S.; Takouchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;
Yasuda, M.; Tabata, S.
#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular
cyanobacterium Synechocystis sp. PCC6803. II. Sequence
determination of the entire genome and assignment of
potential protein-coding regions.
#cross-references MUID:97061201
#accession S75843
#status nucleic acid sequence not shown; translation not shown

##molecule_type DNA
##residues 1-359 ##label KAN
##cross-references EMBL:D90913; GB:AB001339; NID:g1653348; PID:d1019035;
PID:g1653388
##note the nucleotide sequence was submitted to the EMBL Data
Library, June 1996

GENETICS
#start_codon GTG
#superfamily omega-3 fatty acid desaturase
CLASSIFICATION
#oxoreductase
KEYWORDS
#length 359 #molecular-weight 41919 #checksum 9162

Query Match 4.28; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 3,71e-21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPHGWRSHRTH 129
114 ILVPHGWRSHRTH 140

QY 125 ILVPHGWRSHRTH 140

RESULT 13
ENTRY S73778 #type complete
TITLE M2677 homolog Fil.Ofil14 - Mycoplasma pneumoniae (ATCC 29342)
(SGC3)
#formal_name Mycoplasma pneumoniae
ORGANISM ATCC 29342
#variety
DATE 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change
17-Jul-1998

ACCESSIONS
REFERENCE S73778
#authors Hammelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
#journal Nucleic Acids Res. (1996) 24:4420-4449
#title Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
#cross-references M0ID:97105885
#accession S73778
#status preliminary; nucleic acid sequence not shown;
translation not shown

##molecule_type DNA
##residues 1-114 ##label HIM
##cross-references EMBL:AE000044; GB:U00089; NID:g1674130; PID:g1674140
##note the nucleotide sequence was submitted to the EMBL Data
Library, November 1996

GENETICS
#genetic_code SGC3
SUMMARY
#length 114 #molecular-weight 13227 #checksum 9311

Query Match 1.88; Score 7; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 HIKYLI 107
111 HIKYLI 350

QY 344 HIKYLI 350

RESULT 14
ENTRY A70760 #type complete
TITLE hypothetical protein RV2011c - Mycobacterium tuberculosis (strain H37Rv)
ORGANISM #formal_name Mycobacterium tuberculosis
DATE 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998

ACCESSIONS
REFERENCE A70760
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry, III, C.E.; Tekait, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jags, K.; Krogh, A.; McLean, J.; Moule, S.;

Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squires, R.; Stilson, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references M0ID:98295987
#accession A70760
#status preliminary; nucleic acid sequence not shown;
translation not shown

##molecule_type DNA
##residues 1-143 ##label COL
##cross-references GB:U74025; GB:AL123456; NID:g3261586; PID:e248897;
PID:g1403442
##experimental_source strain H37Rv

GENETICS
#gene
SUMMARY
#length 143 #molecular-weight 15725 #checksum 8325

Query Match 1.88; Score 7; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 TSPILV 93
111 TSPILV 239

QY 233 TSPILV 239

RESULT 15
ENTRY B64897 #type complete
TITLE Probable membrane protein b1447 - Escherichia coli
ORGANISM #formal_name Escherichia coli
DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
13-Nov-1998

ACCESSIONS
REFERENCE B64897
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.; Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.; Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao, Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references M0ID:97426617
#accession B64897
#status nucleic acid sequence not shown; translation not shown

##molecule_type DNA
##residues 1-149 ##label BLAT
##cross-references GB:AE000241; GB:U00096; NID:g1787706; PID:g1787718;
UMGF:b1447

##experimental_source strain K-12, substrain MG1655
transmembrane protein

KEYWORDS
FEATURE
3-19 #domain transmembrane #status predicted #label TM1
34-50 #domain transmembrane #status predicted #label TM2
74-90 #domain transmembrane #status predicted #label TM3
100-116 #domain transmembrane #status predicted #label TM4
128-144 #domain transmembrane #status predicted #label TM5

SUMMARY
#length 149 #molecular-weight 15855 #checksum 3006

Query Match 1.88; Score 7; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 3.75e+00;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 39 LINSIVG 45
112 LINSIVG 118

QY 112 LINSIVG 118

Search completed: Sat Aug 21 12:44:01 1999
Job time : 86 secs.

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| FT | TRANSMEM | 55 | 75 | POTENTIAL. |
|-----|----------|---------|-----------|------------------|
| FT | TRANSMEM | 212 | 232 | POTENTIAL. |
| FT | TRANSMEM | 236 | 256 | POTENTIAL. |
| FT | DOMAIN | 100 | 104 | HISTIDINE BOX 1. |
| FT | DOMAIN | 136 | 140 | HISTIDINE BOX 2. |
| FT | DOMAIN | 303 | 307 | HISTIDINE BOX 3. |
| SEQ | SEQUENCE | 380 AA; | 44185 MM; | E3C509B7 CRC32; |

| Query Match | 100.0%; | Score 380; | DB 1; | Length 380; |
|-------------------------------|--------------|------------|---------------|-------------|
| Best Local Similarity 100.0%; | | | | |
| Matches 380; | Conservative | 0; | Mismatches 0; | Indels 0; |

| ID | FD3C SESIN | STANDARD: | PRT: | 447 AA. |
|----|--|-----------|------|---------|
| AC | P46620: | | | |
| DT | 01-FEB-1996 (REL. 33, CREATED) | | | |
| DT | 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) | | | |
| DT | 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) | | | |
| DE | OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-). | | | |
| GN | FAD7 | | | |
| OS | SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY). | | | |
| OC | EUKARYOTA: VIRIDIPHYTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA; | | | |
| OC | EUPHYLLIPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; | | | |
| OC | ASTERIDAE; GENTIANANAE; LAMIALES; PEDALIACEAE; SESAMUM. | | | |
| RN | [1] | | | |
| RC | SEQUENCE FROM N.A. | | | |
| RC | STRAIN-CV. 4294; TISSUE-COTYLEDON; | | | |
| RA | SHOJI K.; | | | |
| RL | SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS. | | | |
| CC | -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES | | | |
| CC | THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY | | | |
| CC | ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT | | | |
| CC | TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS | | | |
| CC | ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. | | | |
| CC | -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. | | | |
| CC | -1- SUBCELLULAR LOCATION: CHLOROPLAST; MEMBRANE-BOUND (PROBABLE). | | | |
| CC | -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE | | | |
| CC | AND/OR BE INVOLVED IN METAL ION BINDING. | | | |
| CC | -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES. | | | |
| CC | ----- | | | |
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CC -----
DR EMBL; U25817; g870784; -.
DR PFAM; PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT FT 1 ? CHLOROPLAST (PORENTAL).
FT CHAIN 2 ? OMEGA-3 FATTY ACID DESATURASE,
FT 1 447 CHLOROPLAST.
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA; 5116 MW; 67B2C46B CRC32.

Query Match 7.6%; Score 29; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 3,13e-63;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 VGHILSSILVPHYGWRISRTHQNQH 212
QY 117 VGHILSSILVPHYGWRISRTHQNQH 145
|||||
RESULT 3 STANDARD; PRT; 404 AA.
ID FD3C_BRANA
AC P48618;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
DE (FRAGMENT).
GN FAD7.
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SEPRANOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; BRASSICA.
[1]
RN RP SEQUENCE FROM N.A.
RP TISSUE-SEED;
RX MEDLINE; 94302147.
RA KYDAN N.S., WIEZBICKI A., AGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ M.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL J., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FLEIDMAN K.A., PIERCE J., BROWSE J.;
RT Cloning of higher plant omega-3 fatty acid desaturases. ;
PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL; L22963; g408490; ALT_INIT.
DR PIR; P00812; P00812.
DR PFAM; PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT FT 1 ?
FT NON_TER 1

```

FT TRANSIT <1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 404 OMEGA-3 FATTY ACID DESATURASE,
CHLOROPLAST.
FT DOMAIN 121 125 HISTIDINE BOX 1.
FT DOMAIN 157 161 HISTIDINE BOX 2.
FT DOMAIN 324 328 HISTIDINE BOX 3.
SQ SEQUENCE 404 AA; 46617 MW; 797F19FB CRC32;
Query Match 7.1%; Score 27; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 8.79e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 316 NIHHDIGTHVHHLFPPQIPHYHLEAT 342
QY 295 NIHHDIGTHVHHLFPPQIPHYHLEAT 321
RESULT 4
ID FD3D_ARATH STANDARD; PRT; 435 AA.
AC P48622;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
DE PRECURSOR (EC 1.14.99.-).
GN FAD8.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLLIPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC CAPPARALES: BRASSICACEAE: ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;
RX MEDLINE: 95148742.
RA KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHWEIGER B., STECCA K.L.,
ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of a temperature-regulated gene encoding a chloroplast
omega-3 desaturase from Arabidopsis thaliana."
RL PLANT PHYSIOL. 106:1615-1621(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RX WATAHIKI M.C., YAMAMOTO K.T.;
RA SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RL FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L27158; G516045; -
DR EMBL: U08216; G457219; -
DR EMBL: D17578; G471093; -
KM OXIDORDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT CHAIN 1 ?
FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT DOMAIN 156 160 DESATURASE, CHLOROPLAST.
FT DOMAIN 192 196 HISTIDINE BOX 1.
FT DOMAIN 192 196 HISTIDINE BOX 2.

FT DOMAIN 359 363 HISTIDINE BOX 3.
SQ SEQUENCE 435 AA; 50136 MW; 70613FE0 CRC32;
Query Match 7.1%; Score 27; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.79e-57;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 351 NIHHDIGTHVHHLFPPQIPHYHLEAT 377
QY 295 NIHHDIGTHVHHLFPPQIPHYHLEAT 321
RESULT 5
ID FD3C_ARATH STANDARD; PRT; 446 AA.
AC P46310;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
DE FAD7 OR FAD8.
GN ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OS CHLOROPLAST.
OC EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLLIPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC CAPPARALES: BRASSICACEAE: ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRU L.,
KINNEY A.J., HITZ W.D., BOOTH J.R., JR., SCHWEIGER B., STECCA K.L.,
ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of a higher plant omega-3 fatty acid desaturases."
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-AERIAL PARTS;
RX MEDLINE: 94043239.
RA IBA K., GIBSON S., NISHITUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
HUGLY S., SOMERVILLE C.R.;
RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and chloroplast
copy number of the fad7 mutant of Arabidopsis thaliana."
RL J. Biol. Chem. 268:24099-24105(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RX WATAHIKI M., YAMAMOTO K.;
RA SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RL FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L22961; G408481; -
DR EMBL: D14007; G541653; -
DR EMBL: D26019; G468434; -

DR PFAM: PF00487; FA.desaturase: 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 2 446 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 163 167 CHLOROPLAST.
 FT DOMAIN 199 203 HISTIDINE BOX 1.
 FT DOMAIN 366 370 HISTIDINE BOX 2.
 FT DOMAIN 366 370 HISTIDINE BOX 3.
 SQ SEQUENCE 446 AA: 51174 MW: 8DE08779 CRC32;

Query Match 7.1% Score 27; DB 1; Length 446;
 Best Local Similarity 100.0%; Pred. No. 8.79e-57;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 NIHHDIGTHVHHLFPOIPHYHVEAT 384
 ||||||||||||||||||||||||||||
 QY 295 NIHHDIGTHVHHLFPOIPHYHVEAT 321

RESULT 6
 ID FD3C-SOYBN STANDARD; PRT; 453 AA.
 AC P48621;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 GN FAD7.
 OS GLYCINE MAX (SOYBEAN).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC FABACEAE; PAPILIONOIDEAE; GLICINE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94302147.
 RA VANDY N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAN L.,
 KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
 ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RT Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L22965; G408792; -.
 DR PFAM: J02339; J02339.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 2 453 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 171 175 CHLOROPLAST.
 FT DOMAIN 207 211 HISTIDINE BOX 1.
 FT DOMAIN 374 378 HISTIDINE BOX 2.
 FT DOMAIN 374 378 HISTIDINE BOX 3.
 SQ SEQUENCE 453 AA: 51362 MW: E4314F1B CRC32;

Query Match 7.1% Score 27; DB 1; Length 453;
 Best Local Similarity 100.0%; Pred. No. 8.79e-57;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 366 NIHHDIGTHVHHLFPOIPHYHVEAT 392
 ||||||||||||||||||||||||||||
 QY 295 NIHHDIGTHVHHLFPOIPHYHVEAT 321

RESULT 7
 ID FD3C-RICCO STANDARD; PRT; 460 AA.
 AC P48619;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
 GN FAD7A-1.
 OS RICINUS COMMUNIS (CASTOR BEAN).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC EUPHORBIALES; EUPHORBIACEAE; RICINUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. BAKER 296; TISSUE-SEED;
 RX MEDLINE: 94302177.
 RA VAN DE LOO F.J., SOMERVILLE C.R.;
 RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
 RL PLANT PHYSIOL. 105:443-444(1994).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L25897; G414732; -.
 DR PFAM: PF00487; FA.desaturase: 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 2 460 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 177 181 CHLOROPLAST.
 FT DOMAIN 213 217 HISTIDINE BOX 1.
 FT DOMAIN 380 384 HISTIDINE BOX 2.
 FT DOMAIN 380 384 HISTIDINE BOX 3.
 SQ SEQUENCE 460 AA: 52561 MW: DB3DA689 CRC32;

Query Match 7.1% Score 27; DB 1; Length 460;
 Best Local Similarity 100.0%; Pred. No. 8.79e-57;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 372 NIHHDIGTHVHHLFPOIPHYHVEAT 398
 ||||||||||||||||||||||||||||
 QY 295 NIHHDIGTHVHHLFPOIPHYHVEAT 321

RESULT 8
 ID FD3E-TOBAC STANDARD; PRT; 379 AA.
 AC P48626;
 DT 01-FEB-1996 (REL. 33, CREATED)

01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
 GN FAD3.
 OS NICOTIANA TABACUM (COMMON TOBACCO).
 CC EUPHAROTIA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 CC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; NICOTIANA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. SRL; TISSUE-LEAF;
 RX MEDLINE; 95011632.
 RA HANADA T., KODAMA H., NISHIMURA M., IBA K.:
 RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
 RL GENE 147:293-294(1994).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D26509; G599592; -;
 DR PFAM; PF00487; FA.desaturase; 1.
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 52 72 POTENTIAL.
 FT TRANSMEM 213 233 POTENTIAL.
 FT TRANSMEM 236 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 SQ SEQUENCE 379 AA; 44149 MW; C237E46D CRC32;
 Query Match 6.6%; Score 25; DB 1; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.09e-50;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 264 KLPYRGKEMSYLRLGGLTVDYDG 288
 QY 267 KLPYRGKEMSYLRLGGLTVDYDG 291
 RESULT 9
 ID FD31_BHRANU STANDARD; PRT; 380 AA.
 AC P32291;
 DT 01-OCT-1993 (REL. 27, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
 GN ARG1.
 OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
 CC EUPHAROTIA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOCOTYL;
 RA YAMAMOTO K.T., MORI H., IMASEKI H.;

"Novel mRNA sequences induced by indole-3-acetic acid in sections of
 RT elongating hypocotyls of mung bean (Vigna radiata).";
 RL PLANT CELL PHYSIOL. 33:13-20(1992).
 CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL; D14410; G287562; -;
 DR PFAM; PF00487; FA.desaturase; 1.
 KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KW TRANSMEMBRANE.
 FT TRANSMEM 59 78 POTENTIAL.
 FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 SQ SEQUENCE 380 AA; 43996 MW; 8429BFB8 CRC32;
 Query Match 6.6%; Score 25; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.09e-50;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 294 HHDIQTHVHHLFQIPHYHLEAT 318
 QY 297 HHDIQTHVHHLFQIPHYHLEAT 321
 RESULT 10
 ID FD31_BHRANU STANDARD; PRT; 377 AA.
 AC P46311;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
 DE (VERSION 1).
 GN FAD3.
 OS BRASSICA NAPUS (RAPE).
 CC EUPHAROTIA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 CC CAPPARIDAE; BRASSICACEAE; BRASSICA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIEZBICKI A., AGERTER M., CASTER C.S., PEREZ-GRU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.:
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER

```
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -----
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
CC EMBL: L22962; GA08492; -.
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 54 73 POTENTIAL.
CC FT TRANSMEM 203 226 POTENTIAL.
CC FT TRANSMEM 233 251 POTENTIAL.
CC FT DOMAIN 92 96 HISTIDINE BOX 1.
CC FT DOMAIN 128 132 HISTIDINE BOX 2.
CC FT DOMAIN 295 299 HISTIDINE BOX 3.
CC SO SEQUENCE 377 AA; 43258 MW; 247237E0 CRC32;

Query Match 6.3%; Score 24; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 3.01e-47;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 287 NIHHDIGTWHHLPQIPHYHLV 310
QY 295 NIHHDIGTWHHLPQIPHYHLV 318

RESULT 11
ID FD32_BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUPHAROTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE:
OC CAPRIFALES; BRASSICACEAE; BRASSICA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HANANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;
RT "Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis."
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -----
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
CC EMBL: L01418; G167148; -.
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 53 73 POTENTIAL.
CC FT TRANSMEM 210 230 POTENTIAL.
CC FT TRANSMEM 234 254 POTENTIAL.
CC FT DOMAIN 98 102 HISTIDINE BOX 1.
CC FT DOMAIN 134 138 HISTIDINE BOX 2.
CC FT DOMAIN 301 305 HISTIDINE BOX 3.
CC SO SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;

Query Match 6.3%; Score 24; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 3.01e-47;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 NIHHDIGTWHHLPQIPHYHLV 316
QY 295 NIHHDIGTWHHLPQIPHYHLV 318

RESULT 12
ID FD3E_ARATH STANDARD; PRT; 386 AA.
AC P48623;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
DE FAD3 OR F23F1.10.
GN ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC EUPHAROTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS; ROSIDAE:
OC CAPRIFALES; BRASSICACEAE; ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA; TISSUE=SEEDLING;
RX MEDLINE: 94302147
RA YADAV N.S., WIENZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases."
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA; TISSUE=HYPOCOTYL;
RA WATAHIKI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA;
RX MEDLINE: 94345020.
RA NISHICHI T., NISHIMURA M., ARONDEL V., IBA K.;
RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
RT fatty acid desaturase from Arabidopsis thaliana."
RL PLANT PHYSIOL. 105:767-768(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN-CV, COLUMBIA;
RA ROUSSEY S.D., LIN X., KENCHUM K.A., CROSBY M.L., BRANDON R.C.,
RA STRES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
```


CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
CC DETECTABLE IN ROOT TISSUE.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22931; G408483; -
CC DR EMBL: D17579; G471091; -
CC DR EMBL: D26508; G1197795; -
CC DR EMBL: AC004680; G3420053; -
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KM OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC TRANSMEMBRANE.
CC FT TRANSMEM 63 83 POTENTIAL.
CC FT TRANSMEM 220 240 POTENTIAL.
CC FT TRANSMEM 242 262 POTENTIAL.
CC FT DOMAIN 101 105 HISTIDINE BOX 1.
CC FT DOMAIN 137 141 HISTIDINE BOX 2.
CC FT DOMAIN 304 308 HISTIDINE BOX 3.
CC SQ SEQUENCE 386 AA; 44076 MW; C228AB8C CRC32;

Query Match 6.3%; Score 24; DB 1; Length 386;
Best Local Similarity 100.0%; Pred. No. 3.01e-47;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 NIHHDICTHVIHLEFPOIPHYLV 319
Y 295 NIHHDICTHVIHLEFPOIPHYLV 318

RESULT 13
ID GR04_NEOCA STANDARD; PRT; 217 AA.
AC P90661; O02507; Q25539;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE DENSE GRANULE PROTEIN PRECURSOR (ANTIGEN NC4.1).
OS NEOSPORA CANINUM.
OC EUKARYOTA; ALVEOLATA; APICOMPLEXA; COCCIDIA; EIMERIIDA; SARCOCYSTIDAE;
OC NEOSPORA.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-NC-1;
RA LALLY N.C., JENKINS M.C., LIDDELL S., DUBEY J.P.;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RP SEQUENCE OF 15-217 FROM N.A.
RC STRAIN-NC-1;
RX MEDLINE: 96336081.
RA LALLY N.C., JENKINS M.C., DUBEY J.P.;
RT "Evaluation of two Neospora caninum recombinant antigens for use in
RT an enzyme-linked immunosorbent assay for the diagnosis of bovine
RT neosporosis."
RL CLIN. DIAGN. LAB. IMMUNOL. 3:275-279(1996).
CC -1- SUBCELLULAR LOCATION: SECRETED (POTENTIAL).
CC -1- SIMILARITY: TO T.GONDI GRAY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL: U72991; G1857224; -
CC DR EMBL: U82229; G2149142; -
CC DR EMBL: U63386; G1353395; -
CC KM ANTIGEN, SIGNAL.
CC FT SIGNAL 1 19 POTENTIAL.
CC FT CHAIN 20 217 DENSE GRANULE PROTEIN.
CC FT CONFLICT 15 18 GLAI -> IRHE (IN REF. 2).
CC SQ SEQUENCE 217 AA; 22495 MW; 104724DB CRC32;

Query Match 2.1%; Score 8; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.85e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 142 IAAIVAAA 149
Y 65 IAAIVAAA 72

RESULT 14
ID HCD2_CAEEL STANDARD; PRT; 309 AA.
AC P41938;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE PROBABLE 3-HYDROXYACYL-COA DEHYDROGENASE B0272.3 (EC 1.1.1.35).
GN B0272.3
OS CAENORHABDITIS ELEGANS.
OC EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
OC RHABDITINA; RHABDITIOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA SUTLSON J.;
RL SUBMITTED (OCT-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
CC NADH.
CC -1- PATHWAY: ONE OF THE ENZYMES OF THE FATTY ACID BETA-OXIDATION
CC CYCLE IN THE MITOCHONDRIA (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
CC -1- SIMILARITY: TO OTHER 3-HYDROXYACYL-COA DEHYDROGENASE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z46240; E1343471; -
CC DR WORMPEP; B0272.3; CE00852.
CC DR PROSITE; PS00067; 3HCDH; 1.
CC DR PFAM: PF00725; 3HCDH; 1.
CC KM HYPOTHETICAL PROTEIN; FATTY ACID METABOLISM; OXIDOREDUCTASE; NAD;
CC KW MITOCHONDRION; MULTIGENE FAMILY.
CC SQ SEQUENCE 309 AA; 33380 MW; D1629EA3 CRC32;

Query Match 2.1%; Score 8; DB 1; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.85e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 285 SPLINSIV 292
Y 110 SPLINSIV 117

RESULT 15
ID Y267_MYCPN STANDARD; PRT; 114 AA.
AC P75397;
DT 01-NOV-1997 (REL. 35, CREATED)

DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL PROTEIN MG267 HOMOLOG.
 OS MYCOPLASMA PNEUMONIAE.
 CC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; MOLICUTES;
 CC MYCOPLASMATACEAE; MYCOPLASMA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE; 97105885.
 RA HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
 RA HERRMANN R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae."
 RL NUCLEIC ACIDS RES. 24:4420-4449(1996).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -----
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 CC -----
 DR EMBL; AE000044; G1674140; -;
 KW HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 75 95 POTENTIAL.
 SQ SEQUENCE 114 AA; 13227 MW; 328665FF CRC32;

Query Match 1.8%; Score 7; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.77e+00;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 101 HLKLYLI 107
 Qy 344 HLKLYLI 350

Search completed: Sat Aug 21 12:44:41 1999
 Job time : 22 secs.

M I P S E R E I H

(TM)

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Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:44:58 1999; MasPar time 22.45 Seconds

Tabular output not generated. 923.998 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Sequence: 1 MYKDTKPLAYANNNGYQKQ.....DTGDVYVYQTDLLHSQRD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: spltembl9

1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.589; Variance 0.470; scale 7.644

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------------------------|-----------|
| 1 | 32 | 8.4 | 436 | 10 | Q40118 DELTA-15 LINEOYL DESAT | 9.72e-66 |
| 2 | 29 | 7.6 | 398 | 10 | Q24626 FATTY ACID DESATURASE | 6.64e-57 |
| 3 | 29 | 7.6 | 438 | 10 | P93452 OMEGA-3 FATTY ACID DES | 6.64e-57 |
| 4 | 29 | 7.6 | 441 | 10 | P93350 OMEGA-3 FATTY ACID DES | 6.64e-57 |
| 5 | 29 | 7.6 | 443 | 10 | O23824 FATTY ACID DESATURASE | 6.64e-57 |
| 6 | 28 | 7.4 | 431 | 10 | O82068 W-3 DESATURASE | 5.50e-54 |
| 7 | 27 | 7.1 | 381 | 10 | P94013 W-3 FATTY ACID DESATUR | 4.42e-51 |
| 8 | 27 | 7.1 | 407 | 10 | O65792 OMEGA-3 FATTY ACID DES | 4.42e-51 |
| 9 | 25 | 6.6 | 438 | 10 | O04807 OMEGA-3 DESATURASE (FR | 4.42e-51 |
| 10 | 25 | 6.6 | 438 | 10 | O04807 OMEGA-3 FATTY ACID DES | 4.42e-51 |
| 11 | 21 | 5.5 | 380 | 10 | O23802 PLASTID OMEGA-3 FATTY | 4.96e-34 |
| 12 | 16 | 4.2 | 359 | 2 | O55240 DELTA-15 DESATURASE | 1.38e-20 |
| 13 | 11 | 2.9 | 350 | 2 | O07872 OMEGA-3 DESATURASE | 3.56e-08 |
| 14 | 8 | 2.1 | 193 | 3 | O74645 FATTY ACID DESATURASE | 8.52e-02 |
| 15 | 7 | 1.8 | 64 | 5 | O46248 HUNCHBACK PROTEIN (FPA | 5.78e+00 |
| 16 | 7 | 1.8 | 152 | 5 | O94519 ACYL-CARRIER SUBUNIT O | 5.78e+00 |
| 17 | 7 | 1.8 | 186 | 2 | O05332 FOF1 ATP SYNTHASE, SUB | 5.78e+00 |
| 18 | 7 | 1.8 | 198 | 2 | O46025 IRON REPRESSIBLE POLYP | 5.78e+00 |
| 19 | 7 | 1.8 | 216 | 5 | O25556 GLUTATHIONE S-TRANSFER | 5.78e+00 |
| 20 | 7 | 1.8 | 257 | 5 | O17734 COSMID C06E7 | 5.78e+00 |

| RESULT | ID | PRELIMINARY | PRT | ALIGNMENTS |
|--------|---|-------------|-----|------------|
| AC | Q40118 | | | |
| DT | 01-NOV-1996 (TREMBL:REL. 01, CREATED) | | | |
| DT | 01-NOV-1996 (TREMBL:REL. 01, LAST SEQUENCE UPDATE) | | | |
| DT | 01-JAN-1999 (TREMBL:REL. 09, LAST ANNOTATION UPDATE) | | | |
| DE | DELTA-15 LINEOYL DESATURASE | | | |
| OS | LIMNANTHES DOUGLASSII | | | |
| OC | EUKARYOTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA: | | | |
| OC | EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE: | | | |
| OC | CAPRALES: LIMNANTHACEAE: LIMNANTHES | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | MEDLINE: 95334518 | | | |
| RX | BHELLA R.S.; MACKENZIE S.L.: | | | |
| RT | "Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding | | | |
| RT | a delta-15 linoleic acid desaturase." | | | |
| RL | PLANT PHYSIOL. 108:861-861(1995). | | | |
| DR | EMBL: U17063; G699390; - | | | |
| DR | PFAM: PF00487; FA_desaturase; 1. | | | |
| DR | MENDEL: 8699; LIMDO:1208:1. | | | |
| SO | SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32; | | | |

| Query Match | Score 32; | DB 10; | Length 436; |
|-------------------------------|---------------------|-----------|-------------|
| Best local Similarity 100.0%; | Pred: No. 9.72e-66; | | |
| Matches 32; Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| Db | 350 | NHHDICGTHVHHPQIPPHHYVATQAAAP | 381 |
|----|-----|------------------------------|-----|
| QY | 295 | NHHDICGTHVHHPQIPPHHYVATQAAAP | 326 |

RESULT 2
AC Q24626; PRELIMINARY; PRT: 398 AA.
DT 01-JAN-1998 (TREMBL:REL. 05, CREATED)
DT 01-JAN-1998 (TREMBL:REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBL:REL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
GN FAD8
OS ZEA MAIZE (MAIZE).
OC EUDAROTA: VIRIDIPHYTES: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA:
OC EUPHYLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: LILIOPSIDA: POALES;
OC POACEAE: ZEA.

[1]
RN SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTAM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -;
DR EMBL: D63953; D1023305; -;
DR PFAM; PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565EEC CRC32;
Query Match 7.6%; Score 29; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 133 VGHILHSSILVPHYHGWRISHRTHQNHGH 161
QY 117 VGHILHSSILVPHYHGWRISHRTHQNHGH 145
RESULT 3
ID P93452 PRELIMINARY; PRT; 438 AA.
AC P93452;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; ANALLALES; APICEAE; PETROSELINUM.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97203190.
RA KIRSCH C., TAKAMIYA-MIK M., REINOLD S., HAHNBROCK K., SOMSSICH I.E.;
RT "Rapid, transient, and highly localized induction of plastidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
DR EMBL; U75745; G1786066; -;
DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9788; PTCr:1208;1.
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 176 VGHILHSSILVPHYHGWRISHRTHQNHGH 204
QY 117 VGHILHSSILVPHYHGWRISHRTHQNHGH 145
RESULT 4
ID P93350 PRELIMINARY; PRT; 441 AA.
AC P93350;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
GN NTFAD7.
OS NICOTIANA TABACUM (COMMON TOBACCO).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANANAE; SOLANALES; SOLANCEAE; NICOTIANA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96416425.
RA HARADA T., NISHIOUCHI T., KODAMA H., NISHIMURA M., IBA K.;
RT "CDNA cloning of a wounding-inducible gene encoding a plastid omega-3
RT fatty acid desaturase from tobacco."
RL PLANT CELL PHYSIOL. 37:606-611(1996).
DR EMBL; D79979; D1012141; -;

DR PFAM; PF00487; FA_desaturase; 1.
DR MENDEL; 9312; Nicta:1208;2.
SQ SEQUENCE 441 AA; 50310 MW; 255F96A6 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 441;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 179 VGHILHSSILVPHYHGWRISHRTHQNHGH 207
QY 117 VGHILHSSILVPHYHGWRISHRTHQNHGH 145
RESULT 5
ID O23824 PRELIMINARY; PRT; 443 AA.
AC O23824;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEA MAYS (MAIZE).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN=HONEY BANTUM;
RX MEDLINE; 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
RT differential expression to temperature."
RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL; D63954; D1023306; -;
DR EMBL; D63952; D1023304; -;
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;
Query Match 7.6%; Score 29; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 6,64e-57;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 178 VGHILHSSILVPHYHGWRISHRTHQNHGH 206
QY 117 VGHILHSSILVPHYHGWRISHRTHQNHGH 145
RESULT 6
ID O82068 PRELIMINARY; PRT; 431 AA.
AC O82068;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUPHAROTIA VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANANAE; SOLANALES; SOLANCEAE; SOLANUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ007739; E1318202; -
SQ SEQUENCE 431 AA; 49253 MW; BAFAP9CD CRC32;

Query Match
Best Local Similarity 100.0%; Score 28; DB 10; Length 431;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 170 GILHSSILVYPYHGMRIHRTHQNHGH 197
118 GILHSSILVYPYHGMRIHRTHQNHGH 145

RESULT 7
ID P94013 PRELIMINARY; PRT: 381 AA.

AC P94013;
DT 01-MAY-1997 (TREMBLERL. 03, CREATED)
DT 01-MAY-1997 (TREMBLERL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLERL. 09, LAST ANNOTATION UPDATE)
DE W-3 FATTY ACID DESATURASE.
OS ORYZA SATIVA (RICE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ORYZA.

RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN-IR36, AND NIPPONBARE;
RA AKAGI H.;
RL SUBMITTED (DEC-1995) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: D78506; G1773736; -
DR EMBL: D78505; G1785856; -
DR MENDEL: 9612; ORYZA;1208;1.
SQ SEQUENCE 381 AA; 43640 MW; 2BD4ED6E CRC32;

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 381;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 290 NIHHDIGTAVIHHLFQIPHYHLVEAT 316
295 NIHHDIGTAVIHHLFQIPHYHLVEAT 321

RESULT 8
ID 065792 PRELIMINARY; PRT: 383 AA.

AC 065792;
DT 01-AUG-1998 (TREMBLERL. 07, CREATED)
DT 01-AUG-1998 (TREMBLERL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLERL. 07, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS GN
GN TAFAD3.
OS TRITICUM AESTIVUM (WHEAT).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.

RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF, AND ROOT;
RA HORIGUCHI G., KAWAKAMI N., KUSUMI K., KODAMA H., IBA K.;
RL PLANT CELL PHYSIOL. 39:540-544(1998).
DR EMBL: D84678; D1029298; -
SQ SEQUENCE 383 AA; 43687 MW; 50D38F40 CRC32;

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 383;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 292 NIHHDIGTAVIHHLFQIPHYHLVEAT 318
295 NIHHDIGTAVIHHLFQIPHYHLVEAT 321

RESULT 9
ID 064907 PRELIMINARY; PRT: 407 AA.

AC 064907;
DT 01-AUG-1998 (TREMBLERL. 07, CREATED)

DT 01-AUG-1998 (TREMBLERL. 07, LAST SEQUENCE UPDATE)

DT 01-AUG-1998 (TREMBLERL. 07, LAST ANNOTATION UPDATE)

DE OMEGA-3 DESATURASE (FRAGMENT).

OS PELARGONIUM X HORTORUM.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC GERANIACEAE; PELARGONIUM.

RP [1]
RP SEQUENCE FROM N.A.
RC SCHULTZ D.J., MUWMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AF020204; G3133289; -
DR NON_TER
SQ SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;

Query Match
Best Local Similarity 100.0%; Score 27; DB 10; Length 407;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 319 NIHHDIGTAVIHHLFQIPHYHLVEAT 345
295 NIHHDIGTAVIHHLFQIPHYHLVEAT 321

RESULT 10
ID 004807 PRELIMINARY; PRT: 438 AA.

AC 004807;
DT 01-JUL-1997 (TREMBLERL. 04, CREATED)
DT 01-JUL-1997 (TREMBLERL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBLERL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PERILLA FROTESCENS.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.

RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OKDONG;
RA LEE S.R., KIM K.H., KIM Y.M., HWANG Y.S.;
RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U59477; G1754795; -
DR PFAM: PF00487; FA.desaturase; 1.
DR MENDEL: 16268; PERFI;1208;mm16268.
SQ SEQUENCE 438 AA; 50160 MW; EE726819 CRC32;

Query Match
Best Local Similarity 100.0%; Score 25; DB 10; Length 438;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 184 LHSSILVYPYHGMRIHRTHQNHGH 208
121 LHSSILVYPYHGMRIHRTHQNHGH 145

RESULT 11
ID 023802 PRELIMINARY; PRT: 380 AA.

AC 023802;
DT 01-JAN-1998 (TREMBLERL. 05, CREATED)
DT 01-JAN-1998 (TREMBLERL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLERL. 08, LAST ANNOTATION UPDATE)
DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
OS TRITICUM AESTIVUM (WHEAT).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; TRITICUM.

RP [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, CHIHOKU; TISSUE-LEAF;
RA HORIGUCHI G., IMAKAWA H., KODAMA H., KAWAKAMI N., NISHIMURA M.,

RA IBA K.; PLANTARUM 96:275-283(1996).
RL PHYSTOL. D43688; D1008371; -.
DR EMBL; D43688; D1008371; -.
PFAM: PF00487; FA_desaturase; 1.
FT NON_TER 1 1
SO SEQUENCE 380 AA; 42633 MW; 2123FF56 CRC32;

Query Match 5.5%; Score 21; DB 10; Length 380;
Best Local Similarity 100.0%; Pred. No. 4,96e-34;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 87 OGTFMALFVLGHDCGHSFS 107
QY 88 OGTFMALFVLGHDCGHSFS 108

RESULT 12
ID 055240; PRELIMINARY; PRT; 359 AA.
AC 055240;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE DELTA 15 DESATURASE.
GN DESB.
OS SYNECHOCYSTIS SP. (STRAIN PCC 6803).
OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCYSTIS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95035996.
RA SAKAMOTO T., LOS D.A., HIGASHI S., WADA H., NISHIDA I., OHMORI M., MURATA N.,
RT "Cloning of omega 3 desaturase from cyanobacteria and its use in altering the degree of membrane-lipid unsaturation.";
RL PLANT MOL. BIOL. 26:249-263(1994).
[2]
RP SEQUENCE FROM N.A.
RA TABATA S.;
RL SUBMITTED (JUN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97061201.
RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y., MIYATAKE N., HIROKAWA M., SUGIURA M., SASAKI S., KIMURA T., HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NAKUO K., OKUMURA S., SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M., TABATA S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
RL DNA RES. 3:109-136(1996).
DR EMBL; D13780; G600598; -.
DR EMBL; D90913; G1653388; -.
PFAM: PF00487; FA_desaturase; 1.
SO SEQUENCE 359 AA; 41919 MW; B5375D98 CRC32;

Query Match 4.2%; Score 16; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1,58e-20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 114 ILVPIYHGMWIRSHRTH 129
QY 125 ILVPIYHGMWIRSHRTH 140

RESULT 13
ID 007872; PRELIMINARY; PRT; 350 AA.
AC 007872;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE OMEGA-3 DESATURASE.
GN DESB.
OS SYNECHOCOCUS PCC7002.

OC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97260123.
RA SAKAMOTO T., BRYANT D.A.;
RT "Temperature-regulated mRNA accumulation and stabilization for fatty acid desaturase genes in the cyanobacterium Synechococcus sp. strain PCC 7002.";
RL MOL. MICROBIOL. 23:1281-1292(1997).
DR EMBL; U36389; G2197199; -.
PFAM: PF00487; FA_desaturase; 1.
SO SEQUENCE 350 AA; 40562 MW; 969CAD61 CRC32;

Query Match 2.9%; Score 11; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 3,56e-08;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 117 HGMWIRSHRTH 127
QY 130 HGMWIRSHRTH 140

RESULT 14
ID 074645; PRELIMINARY; PRT; 193 AA.
AC 074645;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
OS GIBBERELLA ZEA.
OC EUKARYOTA; FUNGI; ASCOMYCOTA; EUASCOMYCETES; PYRENOMYCETES;
OC HYPOCREALES; HYPOCREACEAE; GIBBERELLA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-P15.
RX MEDLINE: 98433864.
RA KIMURA M., MATSUMOTO G., SHINGU Y., YONEYAMA K., YAMAGUCHI I.;
RT "The mystery of the region around Tril101 and acetyltransferase gene. RT Analysis of the region around Tril101 and characterization of its RT homologue from Fusarium sporotrichoides.";
RL FEBS LETT. 435:163-168(1998).
DR EMBL; AB014492; D1034743; -.
FT NON_TER 1 1
FT NON_TER 193 193
SO SEQUENCE 193 AA; 21845 MW; BF2053ED CRC32;

Query Match 2.1%; Score 8; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 8,52e-02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 186 HVYHHLFP 193
QY 303 HVYHHLFP 310

RESULT 15
ID 046248; PRELIMINARY; PRT; 64 AA.
AC 046248;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DE HUNCHBACK PROTEIN (FRAGMENT).
OS DROSOPHILA MIMICA (FRUIT FLY) (IDLOMYIA MIMICA).
OC EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA; PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
OC DROSOPHILIDAE; DROSOPHILA.
RN [1]
RP SEQUENCE FROM N.A.
RA BAKER R.H., DESAILE R.;
RL SYST. BIOL. 46:654-673(1997).
DR EMBL; U93012; G2896866; -.
FT NON_TER 1 1
FT NON_TER 64 64

SQ SEQUENCE 64 AA; 7656 MM; 3A1846DF CRC32;

Query Match 1.8%; Score 7; DB 5; Length 64;

Best Local Similarity 100.0%; Pred. No. 5.78e+00;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

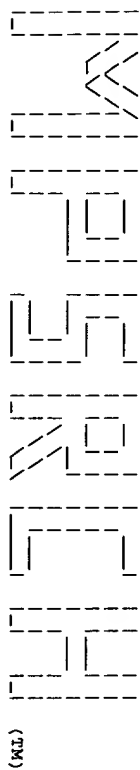
Db 24 HHHGHQ 30

111111

QY 260 HHHGHQ 266

Search completed: Sat Aug 21 12:46:48 1999
Job time : 110 secs.

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(TM)

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March:lp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:38:56 1999; MasPar time 15.00 Seconds

Tabular output not generated. 538.892 Million cell updates/sec

Title: >US-09-219-935-11

Description: (1-380) from US09219935.pep

Sequence: 1 MWKDKRPLAAYANNNGYCKG.....DTGDIVVYVQDTSLILHSQRD 380

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a-genesegs5
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 2.886; Variance 0.710; scale 4.065

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|------------------------|
| 1 | 287 | 75.5 | 380 | 7 | R37595 | Sequence of microsoma |
| 2 | 28 | 7.4 | 447 | 24 | W13381 | Sesame omega-3 allipha |
| 3 | 27 | 7.1 | 378 | 7 | R37591 | Sequence of microsoma |
| 4 | 27 | 7.1 | 404 | 7 | R37594 | Sequence of plasmid d |
| 5 | 27 | 7.1 | 435 | 11 | R60500 | Linoleic-acid-desatur |
| 6 | 27 | 7.1 | 446 | 11 | R60499 | Linoleic-acid-desatur |
| 7 | 27 | 7.1 | 446 | 11 | R37593 | Sequence of a plastid |
| 8 | 27 | 7.1 | 453 | 7 | R37596 | Sequence of soybean P |
| 9 | 24 | 6.3 | 383 | 11 | R60498 | Linoleic-acid-desatur |
| 10 | 24 | 6.3 | 386 | 7 | R37592 | Sequence of delta-15 |
| 11 | 21 | 5.5 | 156 | 7 | R37598 | Sequence of a plastid |
| 12 | 9 | 2.4 | 126 | 7 | R37597 | Sequence of an intern |
| 13 | 8 | 2.1 | 76 | 28 | W37414 | Neospora immunodoma |
| 14 | 8 | 2.1 | 203 | 28 | W31266 | Neospora caninum anti |
| 15 | 8 | 2.1 | 231 | 28 | W38262 | Gliocladium lipolytic |
| 16 | 8 | 2.1 | 232 | 28 | W38263 | Verticillium lipolyti |

| | | | | | | | |
|----|---|-----|------|----|--------|-----------------------|----------|
| 17 | 8 | 2.1 | 232 | 28 | W38264 | Trichophaea saccata 1 | 1.53e+00 |
| 18 | 7 | 1.8 | 20 | 14 | R80294 | Trehalose releasing e | 2.26e+01 |
| 19 | 7 | 1.8 | 224 | 10 | R53701 | Sequence of castor mi | 2.26e+01 |
| 20 | 7 | 1.8 | 302 | 3 | R13512 | P. dentrificans COB V | 2.26e+01 |
| 21 | 7 | 1.8 | 330 | 35 | W59906 | Human HTADXS50 (G-pro | 2.26e+01 |
| 22 | 7 | 1.8 | 330 | 37 | W75245 | Fragment of human sec | 2.26e+01 |
| 23 | 7 | 1.8 | 338 | 17 | R90681 | B. flavum M7-233 RecA | 2.26e+01 |
| 24 | 7 | 1.8 | 382 | 38 | W83353 | Vernonia galamensis | 2.26e+01 |
| 25 | 7 | 1.8 | 383 | 10 | R53698 | Sequence of microsoma | 2.26e+01 |
| 26 | 7 | 1.8 | 383 | 10 | R53697 | Sequence of microsoma | 2.26e+01 |
| 27 | 7 | 1.8 | 384 | 39 | W86154 | Protein sequence of D | 2.26e+01 |
| 28 | 7 | 1.8 | 384 | 39 | W86153 | Protein sequence of F | 2.26e+01 |
| 29 | 7 | 1.8 | 384 | 39 | W86155 | Protein sequence of D | 2.26e+01 |
| 30 | 7 | 1.8 | 384 | 26 | W35136 | Lesquerella fendleri | 2.26e+01 |
| 31 | 7 | 1.8 | 384 | 25 | W24997 | Microsomal delta-12 f | 2.26e+01 |
| 32 | 7 | 1.8 | 384 | 18 | R95579 | Kappa fatty acid hydr | 2.26e+01 |
| 33 | 7 | 1.8 | 384 | 25 | W24995 | Microsomal delta-12 f | 2.26e+01 |
| 34 | 7 | 1.8 | 384 | 25 | W24998 | Microsomal delta-12 f | 2.26e+01 |
| 35 | 7 | 1.8 | 384 | 25 | W24996 | Microsomal delta-12 f | 2.26e+01 |
| 36 | 7 | 1.8 | 387 | 10 | R53702 | Sequence of castor mi | 2.26e+01 |
| 37 | 7 | 1.8 | 597 | 14 | R80290 | Trehalose releasing e | 2.26e+01 |
| 38 | 7 | 1.8 | 598 | 14 | R77471 | Trehalose releasing e | 2.26e+01 |
| 39 | 7 | 1.8 | 761 | 9 | R48036 | Mycobacterium BCG Imm | 2.26e+01 |
| 40 | 7 | 1.8 | 4544 | 9 | R47861 | Alpha 2-Macroglobulin | 2.26e+01 |
| 41 | 7 | 1.8 | 4544 | 11 | R60517 | Human alpha-2-MR. | 2.26e+01 |
| 42 | 6 | 1.6 | 209 | 39 | W84171 | GNFR-alpha protein f | 2.76e+02 |
| 43 | 6 | 1.6 | 294 | 39 | W84169 | GNFR-alpha protein e | 2.76e+02 |
| 44 | 6 | 1.6 | 463 | 39 | W84167 | GNFR-alpha protein e | 2.76e+02 |
| 45 | 6 | 1.6 | 463 | 39 | W84165 | GNFR-alpha protein e | 2.76e+02 |

ALIGNMENTS

RESULT 1
ID R37595 standard; Protein; 380 AA.
AC R37595;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pxfl.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU POINT DE NEMOURS & CO E.I.
PI Browse J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; 043207.
PT Isolated nucleic acid fragment, for plant lipid compn.
PT acid desaturase - comprises nucleic acid sequence encoding fatty
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 144-146; 167pp; English.
CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCR3
CC insert was also used. The identity of the expression product of PCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pxfl was
CC deposited under ATCC 68874.
SQ Sequence 380 AA:
Query Match 75.5%; Score 287; DB 7; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 287; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 94 alf1gndcghgsfstdplnslvghlhasllypyngwrlshthnqngnhiekdesw 153

| | | | |
|----|-----|---|-----|
| Oy | 94 | ALFVLGNHCCGGSGFSDSPLLNSLVGNHLSLIVRUGHWRISNRTNHQNHGIEKDESW | 153 |
| Db | 154 | PLTEKLYHLDASMTFLIRFTFYRFOLFVRYRPLFSGRGRKGSHNRYSLFPSEKRGIA | 213 |
| Oy | 154 | PLTEKTYNNLDSMRKLFEYRPFYRFLYRPLFESRSKGSBSHNPNRYSNLPSEKRGIA | 213 |
| Db | 214 | ISLCLWATMFSLLIYLSFISFISRPILLVLYKLYGIRUYLFYMWALDFVLYLHHBHBKQLPMYRG | 273 |
| Oy | 214 | ISTLCWAMFESLLIYLSFISFISRPILLVLYKLYGIRUYLFYMWALDFVLYLHHNGHNOKLRPMYRG | 273 |
| Db | 274 | KWESYLRGGILCTVARDGVYVLYNHHIDGTYNTHLFPQIRPHRYHVEATGAQRVLGGYUR | 333 |
| Oy | 274 | KWESYLRGGILCTVARDGVYVLYNHHIDGTYNTHLFPQIRPHRYHVEATGAQRVLGGYUR | 333 |
| Db | 334 | EPETSAIRPLRFLIKYLIQASMTQDFIVSDTGCVUYUUCDSLLHNSQGD | 380 |
| Oy | 334 | EPETSAIRPLRFLIKYLIQASMTQDFIVSDTGCVUYUUCDSLLHNSQGD | 380 |

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RESULT 2
ID W13381 standard; Protein; 447 AA.
AC W13381;
DT 02-DEC-1997 (first entry)
DE Sesame omega-3 aliphatic acid desaturase.
KW Sesame; omega-3 aliphatic acid desaturase; modify; fat; oil; plant;
KW linolenic acid; recombinant production.
OS Sesamum indicum.
PN J09065882-A.
PD 11-MAR-1997.
PF 01-SEP-1995; 225145.
PR 01-SEP-1995; JP-225145.
PA (TOYAMA) TOYAMA KEN.
WP: 97-220417/20.
DR N-PSDB; T62066.
PT Sesame omega-3 aliphatic acid desaturase gene - useful in genetic
PT engineering to modify fats and oils in agricultural products
PS Claim 4; Page 4; 10pp; Japanese.
CC This protein is a sesame omega-3 aliphatic acid desaturase. Its coding
CC sequence can be used in genetic engineering to modify fats and oils in
CC agricultural products. The gene or enzyme can be introduced into a plant
CC to modify the aliphatic acid composition in its oils and fats, to give
CC oils and fats with a high content of linolenic acid. Antisense DNA can
CC be introduced into a plant to inhibit the expression of the gene, so
CC that oils and fats with little or no linolenic acid are produced. The
CC gene can also be expressed in microorganisms for recombinant production
CC the enzyme.
SQ Sequence 447 AA;

Query Match 7.4%; Score 28; DB 24; Length 447;
Best Local Similarity 100.0%; Pred. No. 3,89e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 185 ghllhsllvpyhgwrrishrtbhqhnh 212
|||
Oy 118 GHLLHSILVPHYGWRISHRTQHNGH 145

RESULT 3
ID R37591 standard; Protein; 378 AA.
AC R37591;
DT 01-OCT-1993 (first entry)
DE Sequence of microsomal delta-15 glycerolipid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Brassica napus, clone PBNSF3-F2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
PI Browne J, Gau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PT ypadav NS;
WP: w93-197063/24.

```

DR N-BSD8:Q43205.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 136-138: 167pp; English.
CC pcf3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pcf3
CC insert was also used. The identity of the expression product of pcf3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. The cDNA inserts
CC from pcf3 and pcm2 were used to isolate pBNSF3-2. Plasmid pBNSF3-2
CC was deposited as ATCC No. 68854. pBNSF3-3 (Q43206) corresp. to a
CC novel *Brassica napus* seed desaturase different from that shown in
CC Q43205.
SQ Sequence 378 AA;

```

Query Match      7.1%; Score 27; DB 7; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    290 nihhdgcthvnhlfpgdiphyhlveat 316
      |||||
QY    295 NIHHDGCTHVTHHLEPPIPHHYLVEAT 321

RESULT 4
ID     R37594 standard; Protein; 404 AA.
AC     R37594;
DT     01-OCT-1993 (first entry)
DE     Sequence of plastid delta-15 glycerollipid desaturase.
KW     Lipid composition; modification; fatty acid desaturase; enzyme.
OS     Brassica napus, clone pBNSfd-2.
PN     W09311245-A.
PD     10-JUN-1993.
PF     03-DEC-1992; U10284.
PR     04-DEC-1991; US-804259.
PA     (DUPO ) DV POINT DE NEMOURS & CO E. I.
PI     Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI     Yadav NS;
DR     WP1: 93-197063/24.
DR     N-P5DB; Q43206.
PT     Isolated nucleic acid fragment, for plant lipid compsn.
PT     modification - comprises nucleic acid sequence encoding fatty
PT     acid desaturase or related enzyme with high aminoacid identity to
PT     specific polypeptide
PS     Disclosure; Page 140-141; 167pp; English.
PCF3   pcf3 was isolated from a cDNA library using a 5.2 kb Hind III
CC     fragment containing wild-type genomic DNA as a radiolabeled
CC     hybridization probe. One of the sequencing primers made to the PCF3
CC     insert was also used. The identity of the expression product of PCF3
CC     as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC     its biological overexpression in plant tissues. Conserved regions of
CC     R37592 are useful in designing long oligomers for hybridization as
CC     well as shorter ones for use as primers in the PCR. The sequences
CC     of useful regions are given in Q43213-Q43224. The cDNA inserts
CC     from PCF3 and PCM2 were used to isolate pBNSf3-2. Plasmid pBNSf3-2
CC     was deposited at ATCC No. 68854. pBNSfd-3 (Q43206) corresp. to a
CC     novel Brassica napus seed desaturase different from that shown in
CC     Q43205.
SQ     Sequence 404 AA;

Query Match      7.1%; Score 27; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db    316 nihhdgcthvnhlfpgdiphyhlveat 342
      |||||
QY    295 NIHHDGCTHVTHHLEPPIPHHYLVEAT 321
```

RESULT 5
ID R60500 standard; Protein; 435 AA.
AC R60500:
DT 28-MAR-1995 (first entry)
DE Linoletic-acid-desaturase fadD.
KW Linoletic-acid-desaturase; fadD; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PI (UNMS) UNIV MICHIGAN STATE.
PI Atondel VJA, Gibson SI, Kishore GM, Ruff TC, Somerville CR;
DR N-PSDB; 071211.
PT Genetically transformed plants with altered linoletic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 79-81; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 7.1%; Score 27; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 351 nihhdigtvhlhlfpgtphylveat 377
QY 295 NIHHDIGTHVHHLFPGTPHYLVEAT 321

RESULT 6
ID R60499 standard; Protein; 446 AA.
AC R60499:
DT 28-MAR-1995 (first entry)
DE Linoletic-acid-desaturase fadD.
KW Linoletic-acid-desaturase; fadD; transgenic plant; crop improvement;
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PI (UNMS) UNIV MICHIGAN STATE.
PI Atondel VJA, Gibson SI, Kishore GM, Ruff TC, Somerville CR;
DR N-PSDB; 071210.
PT Genetically transformed plants with altered linoletic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoletic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 75-77; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of linoletic-
CC acid-desaturase fadD of Arabidopsis are provided.
SQ Sequence 446 AA;

Query Match 7.1%; Score 27; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 nihhdigtvhlhlfpgtphylveat 384
QY 295 NIHHDIGTHVHHLFPGTPHYLVEAT 321

RESULT 7
ID R37593 standard; Protein; 446 AA.
AC R37593:
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACF2-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; 043204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 132-134; 167p; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to Q43204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of Q43202. R37592 and R37593 show and overall homology of approx.
CC 80%.

Query Match 7.1%; Score 27; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.54e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 nihhdigtvhlhlfpgtphylveat 384
QY 295 NIHHDIGTHVHHLFPGTPHYLVEAT 321

RESULT 8
ID R37596 standard; Protein; 453 AA.
AC R37596:
DT 01-OCT-1993 (first entry)
DE Sequence of soybean plastid delta-15 desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Glycine max, clone pSPD-118bp.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; 043208.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 148-150; 167p; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by

CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Arabidopsis delta-15
CC desaturase cDNA was used as a hybridization probe to isolate a
CC glycerolipid desaturase cDNA from soybean. Plasmid pXFL was
CC deposited under ATCC 68874. Soybean microsomal delta-15
CC desaturase cDNA was used as a hybridization probe to isolate cDNAs
CC encoding related desaturases from soybean. The insert of
CC pSPD-118bp contained a stretch of 1675 nucleotides which contained
CC an open-reading frame encoding a polypeptide (R37596) of about
CC 808 identity with, and colinear with, the Arabidopsis plastid
CC delta-15 desaturase polypeptide listed in R37593. Nucleotides 169
CC to 382 encode the putative plastid transit peptide, colinear with
CC and sharing some homology with the transit peptide described for
CC the Arabidopsis plastid delta-15 glycerolipid desaturase (R37593).
SQ Sequence 453 AA;

Query Match 7.1%; Score 27; DB 7; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.54e-26;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 366 nihndigtvhlhlfpgqiphylveat 392
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLVAT 321

RESULT 9
ID R60498 standard; Protein; 383 AA.
AC R60498:
DT 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase fad3.
KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
KM transgenic plant; crop improvement; yeast artificial chromosome;
KW YAC; linolenic acid.
OS Brassica napus.
PN M09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS.) MONSANTO CO.
PA (UNMS.) UNIV MICHIGAN STATE.
PI Arondei VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI; 94-279758/34.
DR N-PSDB; Q71203.
PT Genetically transformed plants with altered linolenic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure; Page 69-71; 144pp; English.
CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
CC isolated from a YAC library using RFP 220 and ASA2 markers as
CC probes. Isolated DNA was amplified using the primers given in
CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
CC identified in YAC EW7D11.
SQ Sequence 383 AA;

Query Match 6.3%; Score 24; DB 11; Length 383;
Best Local Similarity 100.0%; Pred. No. 8.73e-24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 293 nihndigtvhlhlfpgqiphylv 316
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLV 318

RESULT 10
ID R37592 standard; Protein; 386 AA.
AC R37592;
DT 01-OCT-1993 (first entry)
DE Sequence of delta-15 desaturase.
DE Lipid composition; modification; fatty acid desaturase; enzyme.
KW

OS Arabidopsis thaliana, clone pCF3.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU POINT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43202.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 127-129; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pFdx-2 and
CC pFap7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 5.5%; Score 21; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.19e-19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 296 nihndigtvhlhlfpgqiphylv 319
|||
QY 295 NIHHDIGTHVHLHLPQIPHVHLV 318

RESULT 11
ID R37598 standard; Protein; 156 AA.
AC R37598;
DT 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KM Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone pFdx-2 and pFap7.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO.) DU POINT DE NEMOURS & CO E.I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI; 93-197063/24.
DR N-PSDB; Q43210.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC pCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pCF3
CC insert was also used. The identity of the expression product of pCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pFdx-2 and
CC pFap7. R37598 is a deduced partial peptide sequence of its ORF.
SQ Sequence 156 AA;

Query Match 5.5%; Score 21; DB 7; Length 156;
Best Local Similarity 100.0%; Pred. No. 4.19e-19;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 96 ggtmfwalfvghdcghsfs 116
 |||||||
 OY 88 GGTMFWALFVGHDCGHGSFS 108

RESULT 12
 ID R37597 standard; Protein; 126 AA.
 AC R37597;

DE 01-OCT-1993 (first entry)
 DE Sequence of an internal region of a corn seed delta-15 desaturase.

KM Lipid composition: modification: fatty acid desaturase; enzyme.
 OS zea mays; clone pPCR20.
 PN W09311245-A.

PD 10-JUN-1993.
 PF 03-DEC-1992: U10284.

PR 04-DEC-1991: US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E.I.

PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;

DR WPI: 93-197063/24.
 DR N-PSDB: 043209.

PT Isolated nucleic acid fragment, for plant lipid compn.
 PT modification - comprises nucleic acid sequence encoding fatty

PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide

PS Disclosure: Page 152-153: 167pp: English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III

CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the PCR3

CC insert was also used. The identity of the expression product of PCR3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by

CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as

CC as well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Q43209 is the

CC complete nucleotide sequence of a 396 bp polymerase chain reaction
 CC product derived from corn seed mRNA that is found in the insert of

CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to
 CC the amplification primers described in Q43211 and Q43212

CC respectively. Nucleotides 31 to 363 encode a region that is 61.9%
 CC identical to the region between amino acids 137 and 249 of R37591.

SQ Sequence 126 AA;

Query Match 2.4%; Score 9; DB 7; Length 126;
 Best Local Similarity 100.0%; Pred. No. 8.84e+02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 118 vtylhhgh 126
 |||||||
 OY 256 VTYLHHGH 264

RESULT 13
 ID W37414 standard; Protein; 76 AA.
 AC W37414;

DE 21-MAY-1998 (first entry)
 DE Neospora immunodominant antigen.

KM Immunodominant antigen; abortion; cattle; infection; diagnosis;
 KW Immunodassay; vaccine; protozoan; parasite.

OS Neospora sp.
 PN M09742971-A1.

PD 20-NOV-1997.
 PF 02-MAY-1997: U07500.

PR 10-MAY-1996: US-645951.
 PA (REGC) UNIV CALIFORNIA.

PI Anderson ML, Bair BC, Conrad PA, Louie K, Sverlow KW;
 PI WPI: 98-008582/01.

DR N-PSDB: V00074.
 PT DNA encoding immunodominant antigen of bovine Neospora - used in

PT vaccines and in diagnosis of infection
 PS Claim 2; Page 36; 69pp: English.

CC This protein comprises an immunodominant protein of Neospora that

CC is useful for vaccines and immunodiagnosis of Neospora infection.
 CC The amino acid sequence was deduced from a cDNA clone (see V00074)
 CC isolated from a Neospora bovine strain cDNA library by
 CC immunoscreening with sera from infected cattle. Another
 CC immunodominant protein (see W37413) is also claimed. Also new are:
 CC (1) detection of antibodies (Ab) specific for bovine Neospora
 CC antigen by formation of immune complex between Ab and antigen; (2)
 CC detection of Neospora-specific nucleic acid by hybridisation with a
 CC specific oligonucleotide probe; and (3) a pharmaceutical
 CC composition including bovine Neospora antigen. The methods are
 CC used to diagnose Neospora infection, a major cause of abortion, in
 CC cattle and other animals. Antigens, particularly when expressed by
 CC a recombinant attenuated virus, are used to protect cattle
 CC (especially breeding cows and heifers) against infection.
 SQ Sequence 76 AA;

Query Match 2.1%; Score 8; DB 28; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 laalvaaa 8
 |||||||
 OY 65 IAAVAAA 72

RESULT 14
 ID W31266 standard; Protein; 203 AA.
 AC W31266;

DE 30-APR-1998 (first entry)
 DE Neospora caninum antigenic protein Nc4.1.

KM Neosporosis; antigens; antibodies; mammal; abortion; paralysis.
 OS Neospora caninum.
 PN W09739009-A1.

PD 23-OCT-1997.
 PF 15-APR-1997: U06285.

PR 15-APR-1996: US-624677.
 PA (USDA) US SEC OF AGRIC.

PI Dubley JP, Jenkins MC, Lally NC;
 DR WPI: 97-526385/48.

DR N-PSDB: T89370.
 PT Neospora caninum antigens - useful in assays for diagnosis of

PT neosporosis
 PS Disclosure: Fig 1A; 3pp: English.

CC This is an antigenic protein (Nc4.1) Neospora from caninum, which
 CC contains at least one epitope capable of detecting antibodies to a

CC Neospora sp. Neospora sp. causes neosporosis resulting paralysis and
 CC death in dogs and abortion, neonatal morbidity and mortality in sheep,

CC goats, horses and cattle. The encoded proteins are used in
 CC immunosays (especially ELISA), as reagents for diagnosis of

CC neosporosis in animals, by detecting antibodies to Neospora sp.
 SQ Sequence 203 AA;

Query Match 2.1%; Score 8; DB 28; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 128 laalvaaa 135
 |||||||
 OY 65 IAAVAAA 72

RESULT 15
 ID W38262 standard; Protein; 231 AA.
 AC W38262;

DE 11-MAY-1998 (first entry)
 DE Glucocladium lipolytic enzyme.

KM Lipolytic enzyme; lipase; alkalophilic enzyme; detergent;
 KW surfactant; esterification; lipid hydrolysis;

OS Glucocladium sp. NR140631 (CBS 173.96).
 FH key

FT Peptide 1..31
 /label=sig_peptide

FT Protein 32.231
 FT /Label= Mat_protein
 FT /note= "Claim 1"
 PN W09741212-A1.
 PD 06-NOV-1997.
 PE 22-APR-1997; DK0179.
 PR 25-APR-1996; DK-000501.
 PR 25-APR-1996; DK-000500.
 PA (NOVO) NOVO-NORDISK AS.
 PI Borch K, Halkier T, Hirayama S, Nielsen BR, Oxenboll KM,
 PI Sandal T, Talarar;
 DR WPI; 97-549717/50.
 DR N-PSDB; T95844.
 PT Lipolytic enzymes useful as detergent additives at high pH - from
 PT Gliocladium, Verticillium and Trichophaea genera, give good washing
 PS performance and stability in detergent solutions
 PS Claim 1: Page 37-38; 71pp; English.
 CC This protein comprises an alkalophilic lipase from Gliocladium sp.
 CC isolate N140631. It is characterised as having lipolytic activity
 CC at pH 10 in the absence of Ca²⁺ above 20% of the activity at pH 10
 CC in the presence of 50 mM Ca²⁺, or giving a degree of hydrolysis
 CC above 15% on cotton/Oil swatches in the Activity-in-Detergent
 CC (AID) assay. The enzyme can be produced by cultivation of the
 CC Gliocladium isolate, or by recombinant production in host cells
 CC utilising an isolated DNA sequence (see T95844). Claimed lipases
 CC (see also W38263 and W38264) can be used as detergent additives
 CC (e.g. as non-dusting granulates, stabilised liquids, slurries or
 CC protected enzymes) to remove lipid or fatty stains, and included
 CC with a surfactant in enzymatic detergent compositions (claimed)
 CC e.g. for laundry and dishwashing, especially at high pH. They are
 CC also useful for interesterification, total hydrolysis of fats and
 CC oils and optical isomer resolution.
 SQ Sequence 231 Aa;

Query Match 2.1%; Score 8; DB 28; Length 231;
 Best Local Similarity 100.0%; Pred. No. 1.53e+00;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 146 aalvaal 153
 |||||
 QY 66 AALVAAAI 73

Search completed: Sat Aug 21 12:42:15 1999
 Job time : 199 secs.

NWSEED (TM)

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Mpsrch.p protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:47:05 1999; Maspar time 4.95 Seconds

Tabular output not generated. 779.737 Million cell updates/sec

Title: >US-09-219-935-11
Description: (1-380) from US09219935.pep

Perfect Score: 380
Sequence: 1 MWKDKRPLAYANNGYQQKG.....DTGDVYVYQTDLSLLHSQND 380

Scoring table: TABLE uniprottable
Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 2.726; Variance 0.704; scale 3.871

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-----------------------------------|-----------|
| 1 | 380 | 100.0 | 380 | 3 | PCT-US92-1 Sequence 11, Applicati | 0.00e+00 |
| 2 | 27 | 7.1 | 378 | 3 | PCT-US92-1 Sequence 7, Applicati | 7.27e-28 |
| 3 | 27 | 7.1 | 404 | 3 | PCT-US92-1 Sequence 9, Applicati | 7.27e-28 |
| 4 | 27 | 7.1 | 435 | 3 | PCT-US94-0 Sequence 12, Applicati | 7.27e-28 |
| 5 | 27 | 7.1 | 446 | 3 | PCT-US92-1 Sequence 5, Applicati | 7.27e-28 |
| 6 | 27 | 7.1 | 446 | 3 | PCT-US94-0 Sequence 10, Applicati | 7.27e-28 |
| 7 | 27 | 7.1 | 453 | 3 | PCT-US92-1 Sequence 13, Applicati | 7.27e-28 |
| 8 | 25 | 6.6 | 37 | 2 | US-08-320- Sequence 6, Applicati | 8.09e-25 |
| 9 | 25 | 6.6 | 37 | 1 | US-08-314- Sequence 6, Applicati | 8.09e-25 |
| 10 | 25 | 6.6 | 37 | 1 | US-08-314- Sequence 22, Applicati | 8.09e-25 |
| 11 | 25 | 6.6 | 37 | 2 | US-08-320- Sequence 22, Applicati | 8.09e-25 |
| 12 | 25 | 6.6 | 156 | 3 | PCT-US92-1 Sequence 17, Applicati | 8.09e-25 |
| 13 | 24 | 6.3 | 383 | 3 | PCT-US94-0 Sequence 2, Applicati | 2.64e-23 |
| 14 | 24 | 6.3 | 386 | 3 | PCT-US92-1 Sequence 2, Applicati | 2.64e-23 |
| 15 | 22 | 5.8 | 37 | 1 | US-08-314- Sequence 16, Applicati | 2.67e-20 |
| 16 | 22 | 5.8 | 37 | 1 | US-08-314- Sequence 12, Applicati | 2.67e-20 |
| 17 | 22 | 5.8 | 37 | 2 | US-08-320- Sequence 16, Applicati | 2.67e-20 |
| 18 | 22 | 5.8 | 37 | 2 | US-08-320- Sequence 12, Applicati | 2.67e-20 |
| 19 | 19 | 5.0 | 40 | 2 | US-08-320- Sequence 4, Applicati | 7.41e-16 |
| 20 | 19 | 5.0 | 40 | 2 | US-08-320- Sequence 4, Applicati | 7.41e-16 |
| 21 | 19 | 5.0 | 40 | 1 | US-08-314- Sequence 24, Applicati | 7.41e-16 |
| 22 | 19 | 5.0 | 40 | 1 | US-08-314- Sequence 4, Applicati | 7.41e-16 |
| 23 | 18 | 4.7 | 40 | 1 | US-08-314- Sequence 18, Applicati | 2.14e-14 |

ALIGNMENTS

| RESULT ID | 1 | STANDARD: | PRT: | 380 AA. |
|-----------|---|-----------|------|---------|
| XX | PCT-US92-10284-11 | | | |
| XX | xxxxxx | | | |
| XX | Sequence 11, Application PC/TUS9210284 | | | |
| DE | Sequence 11, Application PC/TUS9210284 | | | |
| XX | Sequence 11, Application PC/TUS9210284 | | | |
| CC | GENERAL INFORMATION: | | | |
| CC | APPLICANT: Browne, John, Kinney, Anthony J., | | | |
| CC | APPLICANT: Pierce, John, Wierzbicki, Anna M., | | | |
| CC | APPLICANT: Yadav, Narendra S., Perez-Grau, Luis | | | |
| CC | TITLE OF INVENTION: Fatty Acid Desaturase Genes | | | |
| CC | NUMBER OF SEQUENCES: 32 | | | |
| CC | CORRESPONDENCE ADDRESS: | | | |
| CC | ADDRESSEE: E. I. du Pont de Nemours and Company | | | |
| CC | STREET: 1007 Market Street | | | |
| CC | CITY: Wilmington | | | |
| CC | STATE: Delaware | | | |
| CC | COUNTRY: U.S.A. | | | |
| CC | ZIP: 19898 | | | |
| CC | COMPUTER READABLE FORM: | | | |
| CC | MEDIUM TYPE: Floppy disk | | | |
| CC | COMPUTER: Macintosh | | | |
| CC | OPERATING SYSTEM: Macintosh System, 6.0 | | | |
| CC | SOFTWARE: Microsoft Word, 4.0 | | | |
| CC | CURRENT APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: PCT/US92/10284 | | | |
| CC | FILING DATE: 19921203 | | | |
| CC | CLASSIFICATION: 435 | | | |
| CC | PRIOR APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: 07/804,259 | | | |
| CC | FILING DATE: 4 DECEMBER 1991 | | | |
| CC | ATTORNEY/AGENT INFORMATION: | | | |
| CC | NAME: Floyd, Linda A. | | | |
| CC | REGISTRATION NUMBER: 33,692 | | | |
| CC | REFERENCE/DOCKET NUMBER: BB-1036-A | | | |
| CC | TELECOMMUNICATION INFORMATION: | | | |
| CC | TELEPHONE: (302) 992-4929 | | | |
| CC | TELEFAX: (302) 892-7949 | | | |
| CC | TELEX: 835420 | | | |
| CC | INFORMATION FOR SEQ ID NO: 11: | | | |
| CC | SEQUENCE CHARACTERISTICS: | | | |
| CC | LENGTH: 380 amino acids | | | |

CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 404 AA; 46617 MW; 906055 CN;

Query Match 7.1%; Score 27; DB 3; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.27e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 316 NIHHDIGTHVHHLFPOIPRHLYEAT 342
|||||
QY 295 NIHHDIGTHVHHLFPOIPRHLYEAT 321

RESULT 4
ID PCT-US94-01321-12 STANDARD; PRT; 435 AA.
XX
AC xxxxxx
XX
DT
XX
XX

Sequence 12, Application PC/TUS9401321

CC Sequence 12, Application PC/TUS9401321
CC GENERAL INFORMATION:

CC APPLICANT:

CC TITLE OF INVENTION: Altered linolenic and linoleic Acid Content

CC TITLE OF INVENTION: In Plants

CC NUMBER OF SEQUENCES: 72

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US94/01321

CC FILING DATE: 04-FEB-1994

CC CLASSIFICATION:

CC PRIOR APPLICATION DATA:

CC FILING DATE: 22-NOV-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/014431

CC FILING DATE: 05-FEB-1993

CC INFORMATION FOR SEQ. ID NO: 12:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 435 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 435 AA; 50136 MW; 1054240 CN;

Query Match 7.1%; Score 27; DB 3; Length 435;
Best Local Similarity 100.0%; Pred. No. 7.27e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 351 NIHHDIGTHVHHLFPOIPRHLYEAT 377
|||||
QY 295 NIHHDIGTHVHHLFPOIPRHLYEAT 321

RESULT 5
ID PCT-US92-10284-5 STANDARD; PRT; 446 AA.
XX
AC xxxxxx
XX
DT
XX
XX

Sequence 5, Application PC/TUS9210284

CC Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:

CC APPLICANT: Browne, John, Kinney, Anthony J.,

CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: E. I. du Pont de Nemours and Company

CC STREET: 1007 Market Street

CC CITY: Wilmington

CC STATE: Delaware

CC COUNTRY: U.S.A.

CC ZIP: 19898

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: Macintosh

CC OPERATING SYSTEM: Macintosh System, 6.0

CC SOFTWARE: Microsoft Word, 4.0

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/10284

CC FILING DATE: 19921203

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 07/804,259

CC FILING DATE: 4 DECEMBER 1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Floyd, Linda A.

CC REGISTRATION NUMBER: 33,692

CC REFERENCE/DOCKET NUMBER: BB-1036-A

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (302) 992-4929

CC TELEFAX: (302) 892-7949

CC TELEX: 835420

CC INFORMATION FOR SEQ. ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 446 amino acids

CC TYPE: AMINO ACID

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

SQ SEQUENCE 446 AA; 51174 MW; 1094717 CN;

Query Match 7.1%; Score 27; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.27e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 358 NIHHDIGTHVHHLFPOIPRHLYEAT 384
|||||
QY 295 NIHHDIGTHVHHLFPOIPRHLYEAT 321

RESULT 6
ID PCT-US94-01321-10 STANDARD; PRT; 446 AA.
XX
AC xxxxxx
XX
DT
XX
XX

Sequence 10, Application PC/TUS9401321
CC GENERAL INFORMATION:

CC APPLICANT:

CC TITLE OF INVENTION: Altered linolenic and linoleic Acid Content

CC TITLE OF INVENTION: In Plants

CC NUMBER OF SEQUENCES: 72

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US94/01321

CC FILING DATE: 04-FEB-1994

CC CLASSIFICATION:

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CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/156551
CC      FILING DATE: 22-NOV-1993
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/014431
CC      FILING DATE: 05-FEB-1993
CC      INFORMATION FOR SEQ ID NO: 10:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 446 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SQ
      Query Match      7.1%; Score 27; DB 3; Length 446;
      Best Local Similarity 100.0%; Freq. No. 7.27e-28;
      Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
      Db      358 NIHHDIGTHVHHLFPLQIPHYHLEAT 384
      Qy      295 NIHHDIGTHVHHLFPLQIPHYHLEAT 321

RESULT
ID      7
AC      PCT-US92-10284-13      STANDARD;      PRT;      453 AA.
XX      xxxxxx
DT
XX
DE      Sequence 13, Application PC/TUS9210284

CC      Sequence 13, Application PC/TUS9210284
CC      GENERAL INFORMATION:
CC      APPLICANT: Browne, John, Kinney, Anthony J.,
CC      APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC      APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC      TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC      TITLE OF INVENTION: from Plants
CC      NUMBER OF SEQUENCES: 32
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: E. I. du Pont de Nemours and Company
CC      STREET: 1007 Market street
CC      CITY: Wilmington
CC      STATE: Delaware
CC      COUNTRY: U.S.A.
CC      ZIP: 19898
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: Macintosh
CC      OPERATING SYSTEM: Macintosh System, 6.0
CC      SOFTWARE: Microsoft Word, 4.0
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US92/10284
CC      FILING DATE: 19921203
CC      CLASSIFICATION: 435
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/804,259
CC      FILING DATE: 4 DECEMBER 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Floyd, Linda A.
CC      REGISTRATION NUMBER: 33,692
CC      REFERENCE/DOCKET NUMBER: BB-1036-A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 13:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 453 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein

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SQ SEQUENCE 453 AA; 51362 MW; 1146882 CN;
  Query Match 7.1%; Score 27; DB 3; Length 453;
  Best Local Similarity 100.0%; Pred. No. 7.27e-28;
  Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 366 NHHDIGTIVIHHLFQPIPHYLVEAT 392
    |||||||
  295 NHHDIGTIVIHHLFQPIPHYLVEAT 321

RESULT 8
ID US-08-320-982-6 STANDARD; PRT; 37 AA.
AC xxxxxx
DT
XX
XX
XX
DE Sequence 6, Application US/08320982
XX
XX Sequence 6, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESSES:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ. ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
  Query Match 6.6%; Score 25; DB 2; Length 37;
  Best Local Similarity 100.0%; Pred. No. 8.09e-25;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Db 1 HHDIGTIVIHHLFQPIPHYLVEAT 25
    |||||||
  QY 297 HHDIGTIVIHHLFQPIPHYLVEAT 321

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ID US-08-314-596-6 STANDARD; PRT; 37 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 6, Application US/08314596
XX
CC Sequence 6, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBAY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314, 596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIGTVIHHLPQIPHYHLEAT 25
YY 297 HHDIGTVIHHLPQIPHYHLEAT 321
RESULT 10
ID US-08-314-596-22 STANDARD; PRT; 37 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 22, Application US/08314596
XX
CC Sequence 22, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBAY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314, 596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIGTVIHHLPQIPHYHLEAT 25
YY 297 HHDIGTVIHHLPQIPHYHLEAT 321
RESULT 11
ID US-08-320-982-22 STANDARD; PRT; 37 AA.
XX
AC xxxxxx
XX
DT
DE Sequence 22, Application US/08320982
XX
CC Sequence 22, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBAY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320, 982

CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4331 MW; 8403 CN;
SQ
Query Match 6.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHDIQTHVHHLFQIPHYHLEAT 25
OY 297 HHDIQTHVHHLFQIPHYHLEAT 321
RESULT 12
ID PCT-US92-10284-17 STANDARD; PRT; 156 AA.
XX AC xxxxxx
XX
XX
XX
DE Sequence 17, Application PC/TUS9210284
XX
CC Sequence 17, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browse, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC OPERATING SYSTEM: Macintosh
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4829
CC TELEFAX: (302) 892-7949

CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pEax-2 and pYacp7
SQ SEQUENCE 156 AA; 17771 MW; 128823 CN;
Query Match 6.6%; Score 25; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 8.09e-25;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 129 LHSILVPHGMRISHRTHQNHG 153
OY 121 LHSILVPHGMRISHRTHQNHG 145
RESULT 13
ID PCT-US94-01321-2 STANDARD; PRT; 383 AA.
XX AC xxxxxx
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XX
XX
XX
DE Sequence 2, Application PC/TUS9401321
CC
CC Sequence 2, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 383 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 383 AA; 43936 MW; 846574 CN;
Query Match 6.3%; Score 24; DB 3; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.64e-23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 293 NIHHDIQTHVHHLFQIPHYHLY 316
OY 295 NIHHDIQTHVHHLFQIPHYHLY 318
RESULT 14

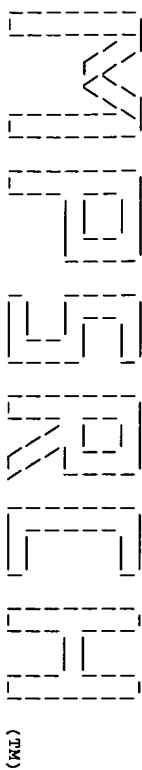
ID PCT-US92-10284-2 STANDARD: PRT: 386 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 2, Application PC/TUS9210284
CC Sequence 2, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browse, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 892-7949
CC TELEFAX: (302) 892-7949
CC CC TELEEX: 835420
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 386 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 386 AA; 44076 MW; 854247 CN;
SQ
Query Match 6.3%; Score 24; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. No. 2,64e-23;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 296 NIHHDIGTHVHHLFPOIPHYHLV 319
|||
QY 295 NIHHDIGTHVHHLFPOIPHYHLV 318

RESULT 15
ID US-08-314-596-16 STANDARD: PRT: 37 AA.
XX
AC xxxxxx
XX
DT
XX
DE Sequence 16, Application US/08314596
CC Sequence 16, Application US/08314596
CC Patent No. 5668292
CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS

CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/314,596
CC FILING DATE: 26-SEP-1994
CC CLASSIFICATION: 435
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 16:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA; 4407 MW; 7119 CN;
SQ
Query Match 5.8%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 2,67e-20;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 HHHDIGTHVHHLFPOIPHYHLV 22
|||
QY 297 HHHDIGTHVHHLFPOIPHYHLV 318

Search completed: Sat Aug 21 12:47:17 1999
Job time : 12 secs.

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:51:01 1999; Maspar time 7.18 Seconds
Tabular output not generated. 703.270 Million cell updates/sec

Title: >US-09-219-935-15
Description: (1-126) from US09219935.pep
Perfect Score: 126
Sequence: 1 HHQNHGHIHDESMHPIREK.....PVLVFMWLDVTLHHHGH 126

Scoring table: TABLE uninterpretable
Gap 60

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 3.217; Variance 0.418; scale 7.697

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|------------------------------|-----------|
| 1 | 16 | 12.7 | 441 | 2 | T03029 omega-3 fatty acid de | 8.02e-23 |
| 2 | 16 | 12.7 | 453 | 2 | J02339 omega-3 fatty acid de | 8.02e-23 |
| 3 | 9 | 7.1 | 377 | 2 | J02337 omega-3 fatty acid de | 2.84e-05 |
| 4 | 9 | 7.1 | 380 | 2 | J02338 omega-3 fatty acid de | 2.84e-05 |
| 5 | 9 | 7.1 | 383 | 2 | A44227 omega-3 fatty acid de | 2.84e-05 |
| 6 | 9 | 7.1 | 385 | 2 | J02335 omega-3 fatty acid de | 2.84e-05 |
| 7 | 9 | 7.1 | 398 | 2 | T01696 omega-3 fatty acid de | 2.84e-05 |
| 8 | 9 | 7.1 | 404 | 2 | P00812 omega-3 fatty acid de | 2.84e-05 |
| 9 | 9 | 7.1 | 443 | 2 | T01697 omega-3 fatty acid de | 2.84e-05 |
| 10 | 9 | 7.1 | 446 | 2 | J02336 omega-3 fatty acid de | 2.84e-05 |
| 11 | 8 | 6.3 | 379 | 2 | J02555 omega-3 fatty acid de | 4.06e-03 |
| 12 | 8 | 6.3 | 1314 | 2 | S19488 probable membrane pro | 4.06e-03 |
| 13 | 7 | 5.6 | 254 | 2 | H69057 hypothetical protein | 4.08e-01 |
| 14 | 7 | 5.6 | 255 | 2 | A13351 probable cobalt ABC t | 4.08e-01 |
| 15 | 7 | 5.6 | 418 | 2 | A64763 probable transport pr | 4.08e-01 |
| 16 | 7 | 5.6 | 419 | 2 | G70602 hypothetical protein | 4.08e-01 |
| 17 | 7 | 5.6 | 570 | 2 | J05722 vacuolar protein sort | 4.08e-01 |
| 18 | 7 | 5.6 | 730 | 2 | A23742 procollagen-lysine 5- | 4.08e-01 |
| 19 | 6 | 4.8 | 27 | 2 | S48878 probable capsid prote | 2.61e+01 |
| 20 | 6 | 4.8 | 121 | 2 | G70469 hypothetical protein | 2.61e+01 |
| 21 | 6 | 4.8 | 289 | 2 | B71243 probable maltose tran | 2.61e+01 |
| 22 | 6 | 4.8 | 293 | 2 | S47094 hypothetical protein | 2.61e+01 |
| 23 | 6 | 4.8 | 294 | 2 | A32377 lymphocyte surface an | 2.61e+01 |

| | | | | | | |
|----|---|-----|------|---|------------------------------|----------|
| 24 | 6 | 4.8 | 312 | 2 | E38245 transcription factor | 2.61e+01 |
| 25 | 6 | 4.8 | 318 | 2 | C38245 transcription factor | 2.61e+01 |
| 26 | 6 | 4.8 | 322 | 2 | I48207 corticotropin-releasi | 2.61e+01 |
| 27 | 6 | 4.8 | 322 | 2 | S13955 corticosteroid-bindin | 2.61e+01 |
| 28 | 6 | 4.8 | 340 | 2 | D38245 transcription factor | 2.61e+01 |
| 29 | 6 | 4.8 | 341 | 2 | A35777 transcription factor | 2.61e+01 |
| 30 | 6 | 4.8 | 345 | 2 | B38245 transcription factor | 2.61e+01 |
| 31 | 6 | 4.8 | 346 | 2 | A38245 transcription factor | 2.61e+01 |
| 32 | 6 | 4.8 | 347 | 2 | A39123 transcription factor | 2.61e+01 |
| 33 | 6 | 4.8 | 359 | 2 | S24240 lymphocyte surface an | 2.61e+01 |
| 34 | 6 | 4.8 | 362 | 2 | A35616 T-cell surface glycop | 2.61e+01 |
| 35 | 6 | 4.8 | 363 | 2 | A37009 CD44 homolog membra | 2.61e+01 |
| 36 | 6 | 4.8 | 365 | 2 | A34424 CD44 membrane glycop | 2.61e+01 |
| 37 | 6 | 4.8 | 367 | 2 | C71357 probable ABC transpor | 2.61e+01 |
| 38 | 6 | 4.8 | 370 | 2 | A71143 hypothetical protein | 2.61e+01 |
| 39 | 6 | 4.8 | 395 | 2 | I77371 CD44R5 - human | 2.61e+01 |
| 40 | 6 | 4.8 | 426 | 2 | JH0518 lymphocyte homing rec | 2.61e+01 |
| 41 | 6 | 4.8 | 436 | 2 | G71152 hypothetical protein | 2.61e+01 |
| 42 | 6 | 4.8 | 503 | 2 | B38745 cell adhesion molecu | 2.61e+01 |
| 43 | 6 | 4.8 | 517 | 2 | B40583 heat shock transcript | 2.61e+01 |
| 44 | 6 | 4.8 | 742 | 2 | A47195 lymphocyte homing rec | 2.61e+01 |
| 45 | 6 | 4.8 | 1160 | 2 | T00272 hypothetical protein | 2.61e+01 |

ALIGNMENTS

RESULT 1
ENTRY T03029 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - common
ORGANISM tobacco
#formal_name Nicotiana tabacum #common_name common tobacco
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

ACCESSIONS
T03029
Z14828
REFERENCE
#authors Hamada, T.; Nishitani, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Plant Cell Physiol. (1996) 37:606-611
#title CDNA cloning of a wounding-inducible gene encoding a plastid
omega-3 fatty acid desaturase from tobacco.

#accession T03029
#status Preliminary: translated from GB/EMBL/DBJ
#molecule_type mRNA
#residues 1-441 #label HAM
#cross-references EMBL:D79979; NID:dt093316; PID:g1694625
#experimental_source cultivar SRI

GENETICS
#gene FAD7
CLASSIFICATION
#superfamily omega-3 fatty acid desaturase
KEYWORDS
#length 441 #molecular_weight 50310 #checksum 6941
SUMMARY

Query Match 12.7%; Score 16; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.02e-23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 311 FVWMLDVTYLLHHGH 326
QY 111 FVWMLDVTYLLHHGH 126

RESULT 2
ENTRY J02339 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
ACCESSIONS
J02339
J02335

#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, R.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.

#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:GMD
#accession JQ2339
##molecule-type mRNA
##residues 1-453 ##label YAD
COMMENT ##cross-references GB:L22965; NID:g408791; PID:g408792
This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast, oxidoreductase
SUMMARY #length 453 #molecular-weight 51362 #checksum 7549

Query Match 12.7%; Score 16; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 8.02e-23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 320 FVWMLDVTYLHHGH 335
|||
QY 111 FVWMLDVTYLHHGH 126

RESULT 3
ENTRY JQ2337 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BN3 - rape
FORMAL_NAME Brassica napus #common_name rape
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS JQ2337
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#contents CDNA:BN3
#accession JQ2337
##molecule-type mRNA
##residues 1-377 ##label YAD
##cross-references GB:L22962; NID:g408491; PID:g408492
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 377 #molecular-weight 43258 #checksum 3294

Query Match 7.1%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 248 VTYLHHGH 256
|||
QY 118 VTYLHHGH 126

RESULT 4
ENTRY JQ2338 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) GW3 - soybean
ORGANISM #formal_name Glycine max #common_name soybean
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999

ACCESSIONS JQ2338
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;

#journal Pierce, J.; Browse, J.
#title Plant Physiol. (1993) 103:467-476
#cross-references MUID:94302147
#accession JQ2338
##molecule-type mRNA
##residues 1-380 ##label YAD
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase; transmembrane protein
SUMMARY #length 380 #molecular-weight 44185 #checksum 1659

Query Match 7.1%; Score 9; DB 2; Length 380;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 256 VTYLHHGH 264
|||
QY 118 VTYLHHGH 126

RESULT 5
ENTRY A44227 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) - rape
ALTERNATE_NAMES omega-3 linoleate desaturase
ORGANISM #formal_name Brassica napus #common_name rape
DATE 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change
20-Mar-1998

ACCESSIONS A44227
REFERENCE A44227
#authors Arondel, V.; Lemieux, B.; Hwang, I.; Gibson, S.; Goodman,
H.M.; Somerville, C.R.
#journal Science (1992) 258:1353-1355
#title Map-based cloning of a gene controlling omega-3 fatty acid
desaturation in Arabidopsis.
#cross-references MUID:93088059
#accession A44227
##status preliminary: not compared with conceptual translation
##molecule-type nucleic acid
##residues 1-383 ##label ARO
##cross-references GB:L01418; NID:g167147; PID:g167148
##experimental_source developing seed
##note sequence extracted from NCBI backbone (NCBI:119842)
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 383 #molecular-weight 43936 #checksum 2897

Query Match 7.1%; Score 9; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 VTYLHHGH 262
|||
QY 118 VTYLHHGH 126

RESULT 6
ENTRY JQ2335 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 -
Arabidopsis thaliana
ORGANISM #formal_name Arabidopsis thaliana #common_name mouse-ear
cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
12-Mar-1999

ACCESSIONS JQ2335
REFERENCE JQ2335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hitz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;

#journal Pierce, J.; Browse, J.
#title Plant Physiol. (1993) 103:467-476
#cross-references EMBL:94302147
#accession J02335
##molecule_type mRNA
##residues 1-386 ##label YAD
REFERENCE
#authors Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.;
Brandon, R.C.; Sykes, S.M.; Kaul, S.; Mason, T.M.;
Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter,
J.C.
#submission submitted to the EMBL Data Library, August 1998
#description Arabidopsis thaliana chromosome II BAC F23F1 genomic
sequence.
#accession T02487
##status translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-386 ##label ROU
##cross-references EMBL:AC004680; NID:g3420043; PID:g3420053
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
GENETICS
#map_position II
#introns 103/2: 133/2; 155/3; 186/3; 248/3; 275/3; 321/3
#exons F23F1.10
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 386 #molecular-weight 44076 #checksum 8044
Query Match 7.1%; Score 9; DB 2; Length 386;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 257 VTYLHHGH 265
OY 118 VTYLHHGH 126
RESULT 7
ENTRY T01696 #type fragment
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD8 - maize
ORGANISM (fragment)
#formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999
ACCESSIONS T01696
REFERENCE 214400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01696
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type mRNA
##residues 1-398 ##label BER
##cross-references EMBL:D63953; NID:d1164452; PID:d1023305
##experimental_source strain honey bantum
GENETICS
#gene FAD8
KEYWORDS oxidoreductase
SUMMARY #length 398 #checksum 5580
Query Match 7.1%; Score 9; DB 2; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 272 VTYLHHGH 280
OY 118 VTYLHHGH 126

RESULT 8
ENTRY PQ0812 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) BND - rape
ORGANISM #formal_name Brassica napus #common_name rape
DATE 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS PQ0812
REFERENCE J02335
#authors Yadau, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browse, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references M01D:94302147
#contents CDNA:BND
#accession PQ0812
##molecule_type mRNA
##residues 1-404 ##label YAD
##cross-references GB:L22963
COMMENT This enzyme introduces the third double bond in the biosynthesis of
18:2 and 18:3 fatty acids which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS chloroplast; oxidoreductase
SUMMARY #length 404 #molecular-weight 46617 #checksum 9400
Query Match 7.1%; Score 9; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 277 VTYLHHGH 285
OY 118 VTYLHHGH 126
RESULT 9
ENTRY T01697 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) FAD7 - maize
ORGANISM #formal_name Zea mays #common_name maize
DATE 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change
19-Feb-1999
ACCESSIONS T01697
REFERENCE 214400
#authors Berberich, T.; Harada, M.; Sugawara, K.; Kodama, H.; Iba, K.;
Kusano, T.
#journal Plant Mol. Biol. (1998) 36:297-306
#title Two maize genes encoding omega-3 fatty acid desaturase and
their differential expression to temperature.
#accession T01697
##status preliminary; translated from GB/EMBL/DBJ
##molecule_type DNA
##residues 1-443 ##label BER
##cross-references EMBL:D63954; NID:d1164453; PID:d1023306
##experimental_source strain honey bantum
GENETICS
#gene FAD7
KEYWORDS oxidoreductase
SUMMARY #length 443 #molecular-weight 49437 #checksum 8872
Query Match 7.1%; Score 9; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 2.84e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 317 VTYLHHGH 325
OY 118 VTYLHHGH 126

RESULT 10
ENTRY J02336 #type complete
TITLE omega-3 fatty acid desaturase (EC 1.14.99.-) CFD -
ORGANISM Arabidopsis thaliana
#formal_name Arabidopsis thaliana #common_name mouse ear
#cross cress
DATE 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change
17-Mar-1999
ACCESSIONS J02336; A49503
REFERENCE J02335
#authors Yadav, N.S.; Wierzbicki, A.; Aegerter, M.; Caster, C.S.;
Perez-Grau, L.; Kinney, A.J.; Hiltz, W.D.; Booth Jr., J.R.;
Schweiger, B.; Stecca, K.L.; Allen, S.M.; Blackwell, M.;
Reiter, R.S.; Carlson, T.J.; Russell, S.H.; Feldmann, K.A.;
Pierce, J.; Browne, J.
#journal Plant Physiol. (1993) 103:467-476
#title Cloning of higher plant omega-3 fatty acid desaturases.
#cross-references MUID:94302147
#accession J02336
#molecule_type mRNA
#residues 1-446 #label YAD
REFERENCE A49503
#authors Iba, K.; Gibson, S.; Nishinchi, T.; Fuse, T.; Nishimura, M.;
Arondel, V.; Hugly, S.; Somerville, C.
#journal J. Biol. Chem. (1993) 268:24099-24105
#title A gene encoding a chloroplast omega-3 fatty acid desaturase
complements alterations in fatty acid desaturation and
chloroplast copy number of the fad7 mutant of Arabidopsis
thaliana.
#cross-references MUID:94043239
#accession A49503
#status preliminary
#molecule_type DNA
#residues 1-446 #label IBA
#note sequence extracted from NCBI backbone (NCBIN:139485,
NCBIRP:139486)
COMMENT The omega-6 and omega-3 fatty acid desaturases introduce the second
and the third double bonds, respectively, in the biosynthesis of
18:2 and 18:3 fatty acids, which are important constituents of
plant membranes.
CLASSIFICATION #superfamily omega-3 fatty acid desaturase
KEYWORDS oxidoreductase
SUMMARY #length 446 #molecular_weight 51174 #checksum 4653
Query Match 7.1%; Score 9; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 2,846-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 319 VTYLHHGH 327
|||
QY 118 VTYLHHGH 126
RESULT 11
ENTRY JC2555 #type complete
TITLE omega-3 fatty acid desaturase - common tobacco (cv. SR1)
ORGANISM #formal_name Nicotiana tabacum #common_name common tobacco
DATE 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change
24-Sep-1998
ACCESSIONS JC2555
REFERENCE JC2555
#authors Hamada, T.; Kodama, H.; Nishimura, M.; Iba, K.
#journal Gene (1994) 147:293-294
#title Cloning of a cDNA encoding tobacco omega-3 fatty acid
desaturase.
#cross-references MUID:95011632
#accession JC2555
#status preliminary
#molecule_type mRNA
#residues 1-379 #label HAM
#cross-references DBJ:026509; NID:g1311180; PID:d1006059; PID:g599592
CLASSIFICATION #superfamily omega-3 fatty acid desaturase

SUMMARY #length 379 #molecular_weight 44149 #checksum 1940
Query Match 6.3%; Score 8; DB 2; Length 379;
Best Local Similarity 100.0%; Pred. No. 4,066-03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 253 VTYLHHGH 260
|||
QY 118 VTYLHHGH 125
RESULT 12
ENTRY S19488 #type complete
TITLE probable membrane protein YCR073c - yeast (Saccharomyces
cerevisiae)
ORGANISM #formal_name Saccharomyces cerevisiae
DATE 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
19-Dec-1997
ACCESSIONS S19488
REFERENCE S19486
#authors Ballester, J.P.G.; Franco, L.; Hoenicka, J.; Jimenez, A.;
Remacha, M.; Sanz, E.
#submission submitted to the Protein Sequence Database, March 1992
#accession S19488
#molecule_type DNA
#residues 1-1314 #label BAL
#cross-references EMBL:X59720; NID:g1907116; PID:g264558; PID:g1907212;
MPS:YCR073c
GENETICS
#map_position 3R
CLASSIFICATION #superfamily unassigned Ser/Thr or Tyr-specific protein
kinases; protein kinase homology
KEYWORDS serine/threonine-specific protein kinase; transmembrane
protein
FEATURE
390-406 #domain transmembrane #status predicted #label TM1\
462-478 #domain transmembrane #status predicted #label TM2\
718-735 #domain transmembrane #status predicted #label TM3\
875-892 #domain transmembrane #status predicted #label TM4\
937-953 #domain transmembrane #status predicted #label TM5\
1032-1310 #domain protein kinase homology #label KIN\
1040-1048 #region protein kinase ATP-binding motif
SUMMARY #length 1314 #molecular_weight 150654 #checksum 4169
Query Match 6.3%; Score 8; DB 2; Length 1314;
Best Local Similarity 100.0%; Pred. No. 4,066-03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 390 LIAFPVYL 397
|||
QY 40 LIAFPVYL 47
RESULT 13
ENTRY H69057 #type complete
TITLE hypothetical protein MTH1434 - Methanobacterium
thermautotrophicum (strain Delta H)
ORGANISM #formal_name Methanobacterium thermotrophicum
DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change
05-Jun-1998
ACCESSIONS H69057
REFERENCE A69000
#authors Smith, D.R.; Doucette-Stamm, L.A.; Delonghery, C.; Lee, H.;
Dubois, J.; Aldredge, T.; Bashirzadeh, R.; Blakey, D.;
Cook, R.; Gilbert, K.; Harrison, D.; Hoang, L.; Keagle, P.;
Lumm, W.; Pothier, B.; Qiu, D.; Spedafora, R.; Vicaltre, R.;
Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; Caruso,
A.; Bush, D.; Saefer, H.; Patwell, D.; Prabhakar, S.;
McDougal, S.; Shimer, G.; Goyal, A.; Pietrowski, S.;
Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling,
J.; Reeve, J.N.
#journal J. Bacteriol. (1997) 179:7135-7155
#title Complete genome sequence of Methanobacterium

thermoautotrophicum Delta H: functional analysis and comparative genomics.
#cross-references MUID:98037514
#accession H69057
#status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-254 ##label MTH
##cross-references GB:AE000905; GB:AE000666; NID:g2622541; PID:g2622546
##experimental_source strain Delta H
GENETICS
#gene MTH434
#start_codon GTG
SUMMARY #length 254 #molecular-weight 28253 #checksum 3627
Query Match 5.6%; Score 7; DB 2; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 220 YGIPYLV 226
|||
QY 104 YGIPYLV 110
RESULT 14
ENTRY A71351 #type complete
TITLE probable cobalt ABC transporter, ATP-binding protein -
ORGANISM syphilis spirochete
#format_name Treponema pallidum subsp. pallidum #common_name
syphilis spirochete
DATE 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
17-Mar-1999
ACCESSIONS A71351
REFERENCE A71250
#authors Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.;
Sutton, G.G.; Dodson, R.; Gwinn, M.; Hickey, E.R.; Clayton,
R.; Ketchum, K.A.; Sodergren, E.; Hardham, J.M.; McLeod,
M.P.; Salzberg, S.; Peterson, J.; Khalak, H.; Richardson,
D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; McDonald,
L.; Artach, P.; Bowman, C.; Cotton, M.D.; Fujii, C.;
Garland, S.; Hatch, B.; Horst, K.; Roberts, K.; Wathey,
L.; Weidman, J.; Smith, H.O.; Venter, J.C.
#journal Science (1998) 281:375-388
#title Complete genome sequence of Treponema pallidum, the syphilis
spirochete.
#cross-references MUID:98332770
#accession A71351
#status preliminary: nucleic acid sequence not shown;
translation not shown
##molecule_type DNA
##residues 1-255 ##label COL
##cross-references GB:AE001204; GB:AE000520; NID:g3322492; PID:g3322495
##experimental_source strain Nichols
GENETICS TP0227
#gene
CLASSIFICATION #superfamily ATP-binding cassette homology
FEATURE 35-217
SUMMARY #domain ATP-binding cassette homology #label ABC
#length 255 #molecular-weight 27321 #checksum 8819
Query Match 5.6%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 104 CAFCPLQ 110
|||
QY 93 CAFCPLQ 99
RESULT 15
ENTRY A64763 #type complete
TITLE probable transport protein mhpT - Escherichia coli
ORGANISM #format_name Escherichia coli

DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
13-Nov-1998
ACCESSIONS A64763
REFERENCE A64720
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kirkpatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession A64763
#status nucleic acid sequence not shown; translation not shown
##molecule_type DNA
##residues 1-418 ##label BLAT
##cross-references GB:AE000142; GB:U00096; NID:g1786542; PID:g1786549;
DMGP:b0353
##experimental_source strain K-12, substrain MG1655
GENETICS
#gene mhpT
KEYWORDS transport protein
FEATURE
28-44 #domain transmembrane #status predicted #label TM1
73-89 #domain transmembrane #status predicted #label TM2
97-113 #domain transmembrane #status predicted #label TM3
126-142 #domain transmembrane #status predicted #label TM4
155-171 #domain transmembrane #status predicted #label TM5
185-201 #domain transmembrane #status predicted #label TM6
234-250 #domain transmembrane #status predicted #label TM7
299-315 #domain transmembrane #status predicted #label TM8
390-406 #domain transmembrane #status predicted #label TM9
SUMMARY #length 418 #molecular-weight 43417 #checksum 3578
Query Match 5.6%; Score 7; DB 2; Length 418;
Best Local Similarity 100.0%; Pred. No. 4.08e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 305 MSLSLA 311
|||
QY 84 MSLSLA 90
Search completed: Sat Aug 21 12:51:23 1999
Job time : 22 secs.

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MSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:51:40 1999; Maspar time 5.02 Seconds

Tabular output not generated. 708,881 Million cell updates/sec

Title: >US-09-219-935-15

Description: (1-126) from US09219935.pep

Sequence: 1 HHQNGHHRDESWHPITEK.....PLVFWMLDLYLHHGH 126

Scoring table: TABLE uniprotatable

Gap 60

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: swiss-prot37

1:swissprot

Statistics: Mean 3.282; Variance 0.391; scale 8.390

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query Length | ID | Description | Pred. No. |
|------------|-------|-------|--------------|------------|-------------------------|-----------|
| 1 | 15 | 12.7 | 453 | PD3C_SOYBN | OMEGA-3 FATTY ACID DES | 6.08e-25 |
| 2 | 15 | 11.9 | 447 | PD3C_SESIN | OMEGA-3 FATTY ACID DES | 4.91e-22 |
| 3 | 9 | 7.1 | 377 | PD31_BRANA | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 4 | 9 | 7.1 | 380 | PD31_SOYBN | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 5 | 9 | 7.1 | 383 | PD32_BRANA | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 6 | 9 | 7.1 | 386 | PD3E_ARATH | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 7 | 9 | 7.1 | 404 | PD3C_BRANA | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 8 | 9 | 7.1 | 435 | PD3D_ARATH | TEMPERATURE-SENSITIVE | 5.59e-06 |
| 9 | 9 | 7.1 | 446 | PD3C_ARATH | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 10 | 9 | 7.1 | 460 | PD3C_RICCO | OMEGA-3 FATTY ACID DES | 5.59e-06 |
| 11 | 8 | 6.3 | 379 | PD3E_TOBAC | OMEGA-3 FATTY ACID DES | 1.15e-03 |
| 12 | 8 | 6.3 | 380 | PD3E_PHAUV | OMEGA-3 FATTY ACID DES | 1.15e-03 |
| 13 | 8 | 6.3 | 1314 | SS22_YEAST | SERINE/THROMBIN PROTE | 1.15e-03 |
| 14 | 7 | 5.6 | 418 | HMPT_ECOLI | POTASSIUM-3-HYDROXYPHEN | 1.60e-01 |
| 15 | 7 | 5.6 | 730 | PLD1_CHICK | PROCOLLAGEN-LYSINE,2-O | 1.60e-01 |
| 16 | 6 | 4.8 | 80 | YAT2_SYNP1 | HYPOTHETICAL 8.8 KD PR | 1.35e+01 |
| 17 | 6 | 4.8 | 83 | YFGJ_ECOLI | HYPOTHETICAL 10 KD PR | 1.35e+01 |
| 18 | 6 | 4.8 | 94 | YOR6_NMV | HYPOTHETICAL 9.2 KD PR | 1.35e+01 |
| 19 | 6 | 4.8 | 119 | YOR6_BACSI | HYPOTHETICAL PROTEIN I | 1.35e+01 |
| 20 | 6 | 4.8 | 214 | YH51_PHAUV | GERMIN-LIKE PROTEIN PR | 1.35e+01 |
| 21 | 6 | 4.8 | 219 | YH51_ARCFU | HYPOTHETICAL PROTEIN A | 1.35e+01 |
| 22 | 6 | 4.8 | 221 | EPD_ESOLU | EPENDYMIN PRECURSOR (E | 1.35e+01 |
| 23 | 6 | 4.8 | 221 | EPD2_SALSA | EPENDYMIN II PRECURSOR | 1.35e+01 |

ALIGNMENTS

| RESULT | ID | STANDARD | PRT | 453 AA. |
|--------|--|----------|-----|---------|
| 1 | PD3C_SOYBN | | | |
| AC | P48621; | | | |
| DT | 01-FEB-1996 (REL. 33, CREATED) | | | |
| DT | 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE) | | | |
| DT | 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) | | | |
| DE | OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-). | | | |
| GN | FMDF. | | | |
| OS | GLYCINE MAX (SOYBEAN). | | | |
| OC | EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES; | | | |
| OC | EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS; ROSIDAE; | | | |
| OC | FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE. | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=SEED; | | | |
| RC | MEDLINE: 94302147. | | | |
| RA | YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L., | | | |
| RA | KINNEY A.J., HITZ M.D., BOOTH J.R., SCHWETGER B., STECCA K.L., | | | |
| RA | ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H., | | | |
| RA | FELDMANN K.A., PIERCE J., BROWSE J.; | | | |
| RT | "Cloning of higher plant omega-3 fatty acid desaturases."; | | | |
| RL | PLANT PHYSIOL. 103:467-476(1993). | | | |
| CC | -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE. INTRODUCTION | | | |
| CC | THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY | | | |
| CC | ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT | | | |
| CC | TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS | | | |
| CC | ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL. | | | |
| CC | -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS. | | | |
| CC | -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE). | | | |
| CC | -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE | | | |
| CC | AND/OR BE INVOLVED IN METAL ION BINDING. | | | |
| CC | -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES. | | | |
| CC | ----- | | | |
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| CC | or send an email to license@isb-sib.ch). | | | |
| CC | ----- | | | |
| DR | EMBL: L22965; G408792; . | | | |
| DR | PIR: JQ2339; JQ2339. | | | |
| DR | PRAM: PF00487; FA_desaturase; 1. | | | |
| DR | OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE; | | | |
| KW | TRANSIT PEPTIDE. | | | |
| FT | TRANSIT 1 ? CHLOROPLAST (POTENTIAL). | | | |

FT CHAIN ? 453 OMEGA-3 FATTY ACID DESATURASE,
FT DOMAIN 171 175 CHLOROPLAST.
FT DOMAIN 207 211 HISTIDINE BOX 1.
FT DOMAIN 374 378 HISTIDINE BOX 2.
FT DOMAIN 374 378 HISTIDINE BOX 3.
SQ SEQUENCE 453 AA: 51362 MW: E4314E1B CRC32;

Query Match 12.7%; Score 16; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 6,08e-25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 320 FVMMDLVLYLHHGH 335
Oy 111 FVMMDLVLYLHHGH 126

RESULT 2
ID FD3C SESIN STANDARD: PRT: 447 AA.

AC P46620: 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7.
OS SESAMUM INDICUM (ORIENTAL SESAME) (GINGELLY).
OC EUDARCTOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; GENTIANANAE; LAMIALES; PEDALIACEAE; SESAMUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. 4294; TISSUE-COTYLEDON;
RA SHOCI K.;

RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 18:3 AND 18:3 FATTY
ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGH
TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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CC or send an email to license@isb-sib.ch).

CC EMBL: U25817; G870784; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KW TRANSIT PEPTIDE.
FT CHAIN 1 ?
FT TRANSIT 1 ?

FT CHAIN 1 ?
FT TRANSIT 1 ?
FT DOMAIN 167 171 HISTIDINE BOX 1.
FT DOMAIN 203 207 HISTIDINE BOX 2.
FT DOMAIN 370 374 HISTIDINE BOX 3.
SQ SEQUENCE 447 AA: 51116 MW: 67B2C46B CRC32;

Query Match 11.9%; Score 15; DB 1; Length 447;
Best Local Similarity 100.0%; Pred. No. 4,91e-22;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VMMDLVLYLHHGH 331
Oy 112 VMMDLVLYLHHGH 126

RESULT 3
ID FD31_BRANA STANDARD: PRT: 377 AA.

AC P46311: 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
(VERSION 1).
GN FAD3.
OS BRASSICA NAPUS (RAPE).
OC EUDARCTOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPPARIDAE; BRASSICACEAE; BRASSICA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SEED;
RX MEDLINE: 94302147.

RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITE W.D., BOOTH J.R., JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
THE THIRD DOUBLBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.

CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.

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CC EMBL: L22962; G408492; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.

FT TRANSMEM 54 73 POTENTIAL.
FT TRANSMEM 203 226 POTENTIAL.
FT TRANSMEM 233 251 POTENTIAL.
FT DOMAIN 92 96 HISTIDINE BOX 1.
FT DOMAIN 128 132 HISTIDINE BOX 2.
FT DOMAIN 295 299 HISTIDINE BOX 3.
SQ SEQUENCE 377 AA: 43258 MW: 247237E0 CRC32;

Query Match 7.1%; Score 9; DB 1; Length 377;
Best Local Similarity 100.0%; Pred. No. 5,59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 248 VTYLHHGH 256
Oy 118 VTYLHHGH 126

RESULT 4
ID FD3E_SOYBN STANDARD: PRT: 380 AA.

AC P46625: 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
GN FAD3.
OS GLYCINE MAX (SOYBEAN).

OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
[1]
RN SEQUENCE FROM N.A.
RC TISSUE-SEED;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.,
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
CC -1- FUNCTION: MICROSOAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L22964; G408794; -
DR PIR: JQ2338; JQ2338.
DR PFAM: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 55 75 POTENTIAL.
FT TRANSMEM 212 232 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT DOMAIN 100 104 HISTIDINE BOX 1.
FT DOMAIN 136 140 HISTIDINE BOX 2.
FT DOMAIN 303 307 HISTIDINE BOX 3.
SQ SEQUENCE 380 AA; 44185 MW; E3C509B7 CRC32;

Query Match 7.1%; Score 9; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 256 VTYLHHGH 264
QY 118 VTYLHHGH 126

RESULT 5
ID FD32.BRANA STANDARD; PRT; 383 AA.
AC P48624;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
DE (VERSION 2).
GN PAD3
OS BRASSICA NAPUS (RAPE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; BRASSICA.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 93088059.
RA ARONDEL V., LEMIEUX B., HWANG I., GIBSON S., GOODMAN H.M.,
RA SOMERVILLE C.R.;

RT Map-based cloning of a gene controlling omega-3 fatty acid
RT desaturation in Arabidopsis.";
RL SCIENCE 258:1353-1355(1992).
CC -1- FUNCTION: ER (MICROSOAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
CC -----
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CC -----
DR EMBL: L01418; G167148; -
DR PIR: PF00487; FA_desaturase; 1.
DR OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
KW TRANSMEMBRANE.
FT TRANSMEM 53 73 POTENTIAL.
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 98 102 HISTIDINE BOX 1.
FT DOMAIN 134 138 HISTIDINE BOX 2.
FT DOMAIN 301 305 HISTIDINE BOX 3.
SQ SEQUENCE 383 AA; 43936 MW; F39A978B CRC32;

Query Match 7.1%; Score 9; DB 1; Length 383;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 VTYLHHGH 262
QY 118 VTYLHHGH 126

RESULT 6
ID FD3E.ARAH STANDARD; PRT; 386 AA.
AC P48623;
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
DE PAD3 OR F23P1.10.
GN ANABIDOPSIS THALIANA (MOOSE-EAR CRESS).
OS EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-SEEDLING;
RX MEDLINE: 94302147.
RA YADAV N.S., WIERZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMAN K.A., PIERCE J., BROWSE J.,
RT Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA; TISSUE-HYPOCOTYL;
RA WATAHITI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
[3]
RN SEQUENCE FROM N.A.

RC STRAIN=CV, COLUMBIA;
 RX MEDLINE; 94345020.
 RA NISHIMUCHI T., NISHIMURA M., ARONDEL V., IBA K.;
 RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
 fatty acid desaturase from Arabidopsis thaliana.";
 RL PLANT PHYSIOL. 105:767-768(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA;
 RA ROUNTSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SKYES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
 CC -1- FUNCTION: MICROSOAM (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
 CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
 CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
 CC PHOSPHOLIPIDS
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND SEEDLINGS. BARELY
 CC DETECTABLE IN ROOT TISSUE.
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL; L22931; G408483; -;
 DR EMBL; D17579; G471091; -;
 DR EMBL; D26508; G1197795; -;
 DR EMBL; AC004680; G3420053; -;
 DR PFM: PF00487; FA.desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
 KM TRANSMEMBRANE.
 FT TRANSMEM 63 83 POTENTIAL.
 FT TRANSMEM 220 240 POTENTIAL.
 FT TRANSMEM 242 262 POTENTIAL.
 FT DOMAIN 101 105 HISTIDINE BOX 1.
 FT DOMAIN 137 141 HISTIDINE BOX 2.
 FT DOMAIN 304 308 HISTIDINE BOX 3.
 FT DOMAIN
 SQ SEQUENCE 386 AA; 44076 MW; C2284B8C CRC32;
 Query Match 7.1%; Score 9; DB 1; Length 386;
 Best Local Similarity 100.0%; Pred. No. 5.59e-06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 257 VTYLHHGH 265
 QY 118 VTYLHHGH 126
 RESULT 7
 ID FD3C.BRANA STANDARD; PRT; 404 AA.
 AC P48618;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-)
 DE (FRAGMENT).
 GN FAD7.
 OS BRASSICA NAPUS (RAPE).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRALES; BRASSICACEAE; BRASSICA.
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=SEED;
 RX MEDLINE; 94302147.
 RA YADAV N.S., WIRZBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
 RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWIEGER B., STECA K.L.,
 RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
 RA FELDMAN K.A., PIERCE J., BROWSE J.;
 RL Cloning of higher plant omega-3 fatty acid desaturases.";
 RL PLANT PHYSIOL. 103:467-476(1993).
 CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
 CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
 CC ACIDS. IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
 CC TO USE PEROXIDIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
 CC ESTERIFIED TO GALCLOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
 CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
 CC AND/OR BE INVOLVED IN METAL ION BINDING.
 CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
 CC -----
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 CC -----
 DR EMBL; L22963; G408490; ALT_INIT.
 DR PIR; P00812; P00812.
 DR PFM: PF00487; FA.desaturase; 1.
 KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
 KM TRANSIT PEPTIDE.
 FT NON TER 1 1
 FT TRANSIT 1 1
 FT CHAIN <1 ? 404
 FT DOMAIN 121 125 CHLOROPLAST (POTENTIAL).
 FT DOMAIN 157 161 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 324 328 CHLOROPLAST.
 FT DOMAIN
 SQ SEQUENCE 404 AA; 46617 MW; 797F19FB CRC32;
 Query Match 7.1%; Score 9; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 5.59e-06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 277 VTYLHHGH 285
 QY 118 VTYLHHGH 126
 RESULT 8
 ID FD3D.ARA7H STANDARD; PRT; 435 AA.
 AC P48622;
 DT 01-FEB-1996 (REL. 33, CREATED)
 DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST
 DE PRECURSOR (EC 1.14.99.-).
 GN FAD8.
 OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
 OC CAPRALES; BRASSICACEAE; ARABIDOPSIS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, COLUMBIA; TISSUE=ARIAL PARTS;
 RX MEDLINE; 95148742.
 RA GIBSON S., ARONDEL V., IBA K., SOMERVILLE C.R.;
 RT "Cloning of a temperature-regulated gene encoding a chloroplast
 RT omega-3 desaturase from Arabidopsis thaliana.";
 RL PLANT PHYSIOL. 106:1615-1621(1994).
 RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA. TISSUE-HYPOCOTYL.
RA WAKAHITI M.C., YAMAMOTO K.T.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- INDUCTION: BY LOW TEMPERATURES.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L27158; G516045; -
DR EMBL: U08216; G497219; -
DR EMBL: D17578; G471093; -
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN 1 ?
FT CHAIN 1 435
FT DOMAIN 156 160
FT DOMAIN 192 196
FT DOMAIN 359 363
SQ SEQUENCE 435 AA: 50136 MW: 70613FE0 CRC32:
Query Match 7.1%; Score 9; DB 1; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 312 VTYLHHGH 320
QY 118 VTYLHHGH 126
RESULT 9
ID FD3C_ARATH STANDARD: PRT: 446 AA.
AC P46310:
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7 OR FADD.
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC CHLOROPLAST.
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC CAPRIFOLIACEAE: BRASSICACEAE: ARABIDOPSIS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA. TISSUE-HYPOCOTYL.
RX MEDLINE: 94302147.
RA YANAV N.S., WIERBICKI A., AEGERTER M., CASTER C.S., PEREZ-GRAU L.,
RA KINNEY A.J., HITZ W.D., BOOTH J.R. JR., SCHWEIGER B., STECCA K.L.,
RA ALLEN S.M., BLACKWELL M., REITER R.S., CARLSON T.J., RUSSELL S.H.,
RA FELDMANN K.A., PIERCE J., BROWSE J.;
RT "Cloning of higher plant omega-3 fatty acid desaturases.";
RL PLANT PHYSIOL. 103:467-476(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA. TISSUE-AERIAL PARTS;
RX MEDLINE: 94043239.

RA IBA K., GIBSON S., NISHIUCHI T., FUSE T., NISHIMURA M., ARONDEL V.,
RA HUGLY S., SOMERVILLE C.R.;
RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
RT complements alterations in fatty acid desaturation and chloroplast
RT copy number of the fad7 mutant of Arabidopsis thaliana.";
RL J. BIOL. CHEM. 268:24099-24105(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA. TISSUE-HYPOCOTYL.
RA WAKAHITI M., YAMAMOTO K.;
RL SUBMITTED (NOV-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN LEAVES AND SEEDLINGS.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
DR EMBL: L22961; G408481; -
DR EMBL: D14007; G541653; -
DR EMBL: D26019; G468434; -
DR PFAM: PF00487; FA_desaturase; 1.
KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
KM TRANSIT PEPTIDE.
FT TRANSIT 1 ?
FT CHAIN 1 446
FT CHAIN 1 446
FT DOMAIN 163 167
FT DOMAIN 199 203
FT DOMAIN 366 370
SQ SEQUENCE 446 AA: 51174 MW: 8DE08779 CRC32:
Query Match 7.1%; Score 9; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 5.59e-06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 319 VTYLHHGH 327
QY 118 VTYLHHGH 126
RESULT 10
ID FD3C_RICCO STANDARD: PRT: 460 AA.
AC P48619:
DT 01-FEB-1996 (REL. 33, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR (EC 1.14.99.-).
GN FAD7A-1.
OS RICINUS COMMUNIS (CASTOR BEAN).
OC EUKARYOTA: VIRIDIPLANTAE: STREPTOPHYTA: EMBRYOPHYTA: TRACHEOPHYTA;
OC EUPHYLLOPHYTES: SPERMATOPHYTA: MAGNOLIOPHYTA: EUDICOTYLEDONS: ROSIDAE;
OC EUPHORBIACEAE: EUPHORBIACEAE: RICINUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. BAKER 296; TISSUE-SEED.
RX MEDLINE: 94302177.
RA VAN DE LOO F.J., SOMERVILLE C.R.;
RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.";
RL PLANT PHYSIOL. 105:443-444(1994).

CC -1- FUNCTION: CHLOROPLAST OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 16:3 AND 18:3 FATTY
CC ACIDS, IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT
CC TO USE FERREDOXIN AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO GALACTOLIPIDS, SULFOLIPIDS AND PHOSPHATIDYLGLYCEROL.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC -----
CC EMBL: L25897; G414732; -
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; CHLOROPLAST; MEMBRANE;
CC FT TRANSIT PEPTIDE.
CC KM
CC FT CHAIN 1 ? ? CHLOROPLAST (POTENTIAL).
CC FT DOMAIN 177 181 CHLOROPLAST.
CC FT DOMAIN 213 217 HISTIDINE BOX 1.
CC FT DOMAIN 384 384 HISTIDINE BOX 2.
CC FT DOMAIN 52561 52561 MW; DB3DA689 CRC32;
CC SQ SEQUENCE 460 AA; DB3DA689 CRC32;
CC
CC Query Match 7.1%; Score 9; DB 1; Length 460;
CC Best Local Similarity 100.0%; Pred. No. 5.59e-06;
CC Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 333 VTYLHHHG 341
CC 118 VTYLHHHG 126
CC
CC RESULT 11
CC ID FD3E_TOBAC STANDARD; PRT: 379 AA.
CC AC P48626;
CC DT 01-FEB-1996 (REL. 33, CREATED)
CC DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
CC DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
CC DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-).
CC GN FAD3.
CC OS NICOTIANA TABACUM (COMMON TOBACCO).
CC OC EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
CC OC ASTRIDALES; SOLANACEAE; SOLANACEAE; NICOTIANA.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN-CV. SRL: TISSUE-LEAF.
CC RX MEDLINE: 95011632.
CC RA HAMADA T., KODAMA H., NISHIMURA M., IBA K.;
CC RT "Cloning of a cDNA encoding tobacco omega-3 fatty acid desaturase.";
CC RL GENE 147:293-294(1994).
CC CC -1- FUNCTION: ER (MICROSOMAL) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D14410; G287562; -
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC FT TRANSMEM
CC FT TRANSMEM 59 78 POTENTIAL.

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CC -----
CC EMBL: D26509; G599592; -
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC FT TRANSMEM 52 72 POTENTIAL.
CC FT TRANSMEM 213 233 POTENTIAL.
CC FT TRANSMEM 236 256 POTENTIAL.
CC FT DOMAIN 97 101 HISTIDINE BOX 1.
CC FT DOMAIN 133 137 HISTIDINE BOX 2.
CC FT DOMAIN 300 304 HISTIDINE BOX 3.
CC SQ SEQUENCE 379 AA; 44149 MW; C237464D CRC32;
CC
CC Query Match 6.3%; Score 8; DB 1; Length 379;
CC Best Local Similarity 100.0%; Pred. No. 1.15e-03;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Db 253 VTYLHHHG 260
CC 118 VTYLHHHG 125
CC
CC RESULT 12
CC ID FD3E_PHAUG STANDARD; PRT: 380 AA.
CC AC P32291;
CC DT 01-OCT-1993 (REL. 27, CREATED)
CC DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
CC DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
CC DE OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (EC 1.14.99.-)
CC (INDOLE-3-ACETIC ACID INDUCED PROTEIN ARG1).
CC GN ARG1.
CC OS PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA).
CC OC EUKARYOTA; VIRIDIPHYTES; EMBRYOPHYTA; TRACHEOPHYTA;
CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
CC OC FABALES; FABACEAE; PAPILIONOIDEAE; VIGNA.
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE-HYPOCOTYL.
CC RA YAMAMOTO K.T., MORI H., IMASEKI H.;
CC RT "Novel mRNA sequences induced by indole-3-acetic acid in sections of
CC elongating hypocotyls of mung bean (Vigna radiata).";
CC RL PLANT CELL PHYSIOL. 33:13-20(1992).
CC CC -1- FUNCTION: MICROSOMAL (ER) OMEGA-3 FATTY ACID DESATURASE INTRODUCES
CC THE THIRD DOUBLEBOND IN THE BIOSYNTHESIS OF 18:3 FATTY ACIDS,
CC IMPORTANT CONSTITUENTS OF PLANT MEMBRANES. IT IS THOUGHT TO USE
CC CYTOCHROME B5 AS AN ELECTRON DONOR AND TO ACT ON FATTY ACIDS
CC ESTERIFIED TO PHOSPHATIDYLCHOLINE AND, POSSIBLY, OTHER
CC PHOSPHOLIPIDS.
CC -1- PATHWAY: POLYUNSATURATED FATTY ACID BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM.
CC -1- INDUCTION: BY AUXIN, ETHYLENE AND WOUNDING.
CC -1- DOMAIN: THE HISTIDINE BOX DOMAINS MAY CONTAIN THE ACTIVE SITE
CC AND/ OR BE INVOLVED IN METAL ION BINDING.
CC -1- SIMILARITY: TO OTHER PLANT OMEGA-3 FATTY ACID DESATURASES.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D14410; G287562; -
CC DR PFAM: PF00487; FA_desaturase; 1.
CC KW OXIDOREDUCTASE; FATTY ACID BIOSYNTHESIS; ENDOPLASMIC RETICULUM;
CC FT TRANSMEM 59 78 POTENTIAL.

FT TRANSMEM 208 231 POTENTIAL.
 FT TRANSMEM 238 256 POTENTIAL.
 FT DOMAIN 97 101 HISTIDINE BOX 1.
 FT DOMAIN 133 137 HISTIDINE BOX 2.
 FT DOMAIN 300 304 HISTIDINE BOX 3.
 SO SEQUENCE 380 AA: 43996 MW: 8429868 CRC32:

Query Match 6.38; Score 8; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 1.15e-03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 253 VTYLHHHG 260
 11111111
 118 VTYLHHHG 125

Query Match 6.38; Score 8; DB 1; Length 380;
 Best Local Similarity 100.0%; Pred. No. 1.15e-03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
 ID SS22_YEAST STANDARD; PRT; 1314 AA.
 AC P25390;
 DT 01-MAY-1992 (REL. 22, CREATED)
 DT 01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
 DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
 DE SERINE/THREONINE PROTEIN KINASE SSK22 (EC 2.7.-.-).
 GN SSK22 OR YCR073C OR YCR73C.
 OS SACCAROMYCES CEREVISIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOCETES; SACCAROMYCETALES;
 OC SACCAROMYCETACEAE; SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BALLESTA J.P.G., FRANCO L., HOENICKA J., JIMENEZ A., REMACHA M.,
 RA SANZ E.;
 RL SUBMITTED (MAR-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE: 95350642.
 RA MAEDA T., TAKEMAWA M., SAITO H.;
 RT "Activation of yeast PBS2 MAPK by MAPKKs or by binding of an SH3-
 containing osmosensor."
 RL SCIENCE 269:554-558(1995).
 CC -1- FUNCTION: KINASE INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
 ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE EXTRACELLULAR
 ENVIRONMENT. ACTIVATES THE PBS2 MAP KINASE BY
 PHOSPHORYLATION.
 CC -1- SUBUNIT: INTERACTS WITH BY SSK1.
 CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 PROTEIN KINASES. BELONGS TO THE MAP KINASE KINASE FAMILY.
 CC
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 CC
 CC EMBL: X59720; E264558; -
 DR PIR: S19488; S19488.
 DR SGD: L0002827; SSK22.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PFAM: PF00069; PKinase; 1.
 DR HSP: P24941; IAO1.
 KM TRANSFERASE: SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
 FT DOMAIN 1034 1314
 FT NP_BIND 1040 1048 ATP (BY SIMILARITY).
 FT BINDING 1063 1063 ATP (BY SIMILARITY).
 FT ACT_SITE 1158 1158 BY SIMILARITY.
 SO SEQUENCE 1314 AA: 150654.MW: 1473178 CRC32:

Query Match 6.38; Score 8; DB 1; Length 1314;
 Best Local Similarity 100.0%; Pred. No. 1.15e-03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 390 LLAFPVYL 397
 11111111
 40 LLAFPVYL 47

Query Match 6.38; Score 8; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.15e-03;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 ID MHPT_ECOLI STANDARD; PRT; 418 AA.
 AC P77589; P77037;
 DT 01-NOV-1997 (REL. 35, CREATED)
 DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE PUTATIVE 3-HYDROXYPHENYLPROBIONIC ACID TRANSPORTER.
 GN MHPT.
 OS ESCHERICHIA COLI.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 OC ESCHERICHIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE: 97426617.
 RA BLATTNER F.R., PLUNKERT G., III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER E.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL SCIENCE 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA DUNCAN M., ALLEN E., ARAUJO R., APARICIO A.M., CHUNG E., DAVIS K.,
 RA FEDERSPIEL N., HYMAN R., KALMAN S., KOMP C., KURDI O., LEW H., LIN D.,
 RA NAMATH A., OEFNER P., ROBERTS D., SCHRAMM S., DAVIS R.W.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA NASHIMOTO H., SAITO N.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE OF 98-345 FROM N.A.
 RC STRAIN-K12 / CS520;
 RA FERRANDEZ A., GARCIA J.L., DIAZ E.;
 RL SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -1- FUNCTION: COULD BE A TRANSPORTER FOR 3-PHENYLPROPIONATE
 (HYDROCCINNAMIC ACID).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
 (POTENTIAL).
 CC
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 CC
 CC EMBL: AE000142; G1786549; -
 DR EMBL: U73857; G1657549; -
 DR EMBL: D85613; -; NOT ANNOTATED_CDS.
 DR EMBL: X97543; E242997; -
 DR ECOGENE: EGI3293; MHPT.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; 1.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; 1.
 DR PFAM: PF00083; sugar tr; 1.
 KM TRANSPORT: TRANSMEMBRANE, INNER MEMBRANE, SYMPORT.
 FT TRANSMEM 32 52 POTENTIAL.
 FT TRANSMEM 69 89 POTENTIAL.
 FT TRANSMEM 97 117 POTENTIAL.
 FT TRANSMEM 121 141 POTENTIAL.
 FT TRANSMEM 158 178 POTENTIAL.

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FT TRANSMEM 180 200 POTENTIAL.
FT TRANSMEM 233 253 POTENTIAL.
FT TRANSMEM 269 289 POTENTIAL.
FT TRANSMEM 295 315 POTENTIAL.
FT TRANSMEM 322 342 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
FT TRANSMEM 385 405 POTENTIAL.
FT CONFLICT 310 310 L -> V (IN REF. 4).
SQ SEQUENCE 418 AA; 43417 MW; AE3D1B8F CRC32;

Query Match 5.6%; Score 7; DB 1; Length 418;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 305 MLASILA 311
QY 84 MLASILA 90

RESULT 15
ID PLO1_CHICK STANDARD; PRT: 730 AA.
AC P24802;
DT 01-MAR-1992 (REL. 21, CREATED)
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
DT 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE PROCOLLAGEN-LYSINE,2-OKOGLUTARATE 1 PRECURSOR
DE (EC 1.14.11.4) (LYSL HYDROXYLASE 1) (LH1).
GN PLOD1 OR PLOD.
OS GALLUS GALLUS (CHICKEN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; ARCHOSAURIA; AVES;
OC NEOGNATHAE; GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-40; 412-417; 508-515 & 550-573.
RX MEDLINE; 9131570.
RA KIVIRIKKO K.I., TURPENNIEMI-HUJANEN T., PAJUNEN L.,
RA PIHLAJANIEMI T., MYLLYLA R.;
RT "Molecular cloning of chick lysyl hydroxylase. Little homology in
RT primary structure to the two types of subunit of prolyl
RT 4-hydroxylase."
RL J. BIOL. CHEM. 266:2805-2810(1991).
CC -1- FUNCTION: FORMS HYDROXYLYSINE RESIDUES IN -XAA-LYS-GLY- SEQUENCES
CC IN COLLAGENS. THESE HYDROXYLYSINES SERVE AS SITES OF ATTACHMENT
CC FOR CARBOHYDRATE UNITS AND ARE ESSENTIAL FOR THE STABILITY OF THE
CC INTERMOLECULAR COLLAGEN CROSSLINKS.
CC -1- CATALYTIC ACTIVITY: PROCOLLAGEN L-LYSINE + 2-OKOGLUTARATE + O(2) =
CC PROCOLLAGEN 5-HYDROXY-L-LYSINE + SUCCINATE + CO(2).
CC -1- COFACTOR: REQUIRES IRON AND ASCORBATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND IN CISTERNAE OF ROUGH
CC ENDOPLASMIC RETICULUM.
CC -1- SIMILARITY: BELONGS TO THE LYSYL HYDROXYLASE FAMILY.
CC -----
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CC -----
DR EMBL: M59183; G212282; -
DR PTR: A23742; A23742; -
DR PROSITE: PS01325; LYS_HYDROXYLASE; 1.
KW OXIDOREDUCTASE; DIOXYGENASE; SIGNAL; IRON; VITAMIN C; GLYCOPROTEIN;
KW ENDOPLASMIC RETICULUM; MEMBRANE.
FT SIGNAL 1 20
FT CHAIN 21 730 LYSYL HYDROXYLASE 1.
FT METAL 659 659 IRON (BY SIMILARITY).
FT METAL 661 661 IRON (BY SIMILARITY).
FT METAL 711 711 IRON (BY SIMILARITY).
FT ACT_SITE 721 721 POTENTIAL.
FT CARBOHYD 200 200 POTENTIAL.
FT CARBOHYD 403 403 POTENTIAL.
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FT CARBOHYD 541 541 POTENTIAL.
FT CARBOHYD 689 689 POTENTIAL.
SQ SEQUENCE 730 AA; 84318 MW; B2A6C014 CRC32;

Query Match 5.6%; Score 7; DB 1; Length 730;
Best Local Similarity 100.0%; Pred. No. 1.60e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 625 PITEKLY 631
QY 16 PITEKLY 22

Search completed: Sat Aug 21 12:51:58 1999
Job time : 18 secs.
```

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W E I R E D (TM)

Msearch - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:52:15 1999; Maspar time 9.96 Seconds
690.478 Million cell updates/sec

Tabular output not generated.

Title: >US-09-219-935-15
Description: (1-126) from US09219935.pep
Perfect Score: 126
Sequence: 1 HHQNHGTHRDESMHPIEK.....PVLVFMVMDLVLYLHHGH 126

Scoring table: TABLE uniprottable
Gap 60

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human
5:sp.invertebrate 6:sp.mammal 7:sp.mhc 8:sp.organelle
9:sp.phage 10:sp.plant 11:sp.rodent 12:sp.unclassified
13:sp.vertebrate 14:sp.virus

Statistics: Mean 3.195; Variance 0.413; scale 7.739

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description | Pred. No. |
|------------|-------|-------------|--------|--------|------------------------|-----------|
| 1 | 20 | 15.9 | 381 10 | P94013 | W-3 FATTY ACID DESATUR | 4.43e-34 |
| 2 | 16 | 12.7 | 441 10 | P93350 | OMEGA-3 FATTY ACID DES | 6.47e-23 |
| 3 | 15 | 11.9 | 383 10 | 065792 | OMEGA-3 FATTY ACID DES | 3.26e-20 |
| 4 | 13 | 10.3 | 438 10 | 004807 | OMEGA-3 FATTY ACID DES | 6.00e-15 |
| 5 | 10 | 7.9 | 350 2 | 007872 | OMEGA-3 DESATURASE. | 1.58e-07 |
| 6 | 9 | 7.1 | 380 10 | 023802 | PLASTID OMEGA-3 FATTY | 3.12e-05 |
| 7 | 9 | 7.1 | 398 10 | 024626 | FATTY ACID DESATURASE | 3.12e-05 |
| 8 | 9 | 7.1 | 407 10 | 064907 | OMEGA-3 DESATURASE (FR | 3.12e-05 |
| 9 | 9 | 7.1 | 431 10 | 082068 | W-3 DESATURASE. | 3.12e-05 |
| 10 | 9 | 7.1 | 438 10 | P93452 | OMEGA-3 FATTY ACID DES | 3.12e-05 |
| 11 | 9 | 7.1 | 443 10 | 023824 | FATTY ACID DESATURASE. | 3.12e-05 |
| 12 | 7 | 5.6 | 254 1 | 027483 | HYPOTHETICAL 28.3 KD P | 4.90e-01 |
| 13 | 7 | 5.6 | 255 2 | 083255 | COBALT ABC TRANSPORTER | 4.90e-01 |
| 14 | 7 | 5.6 | 419 2 | 005589 | HYPOTHETICAL 38.8 KD P | 4.90e-01 |
| 15 | 7 | 5.6 | 436 10 | 040118 | DELTA-15 LINOLYL DESAT | 4.90e-01 |
| 16 | 7 | 5.6 | 570 11 | 008700 | RVP845 | 4.90e-01 |
| 17 | 7 | 5.6 | 570 11 | P97390 | VACUOLAR PROTEIN SORTI | 4.90e-01 |
| 18 | 7 | 5.6 | 570 11 | 015715 | VACUOLAR PROTEIN SORTI | 4.90e-01 |
| 19 | 6 | 4.8 | 135 14 | 091954 | POLYPROTEIN (FRAGMENT) | 3.28e+01 |
| 20 | 6 | 4.8 | 157 4 | Q15619 | PUTATIVE OLFACTORY REC | 3.28e+01 |

| RESULT ID | AC | ID | Score | Query Match | Length | DB ID | Description | Pred. No. |
|-----------|--------|--------|-------|-------------------------------|---------------------|-------|------------------------|---|
| 1 | P94013 | P94013 | 15.98 | Score 20: | DB 10: | 241 | PVLVFMVMDLVLYLHHGH 260 | 100.08; Pred. No. 4.43e-34; |
| 2 | P94013 | P94013 | 12.7 | Best Local Similarity 100.08; | Pred. No. 4.43e-34; | 107 | PVLVFMVMDLVLYLHHGH 126 | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |

ALIGNMENTS

| RESULT ID | AC | ID | Score | Query Match | Length | DB ID | Description | Pred. No. |
|-----------|--------|--------|-------|-------------------------------|---------------------|-------|------------------------|---|
| 1 | P94013 | P94013 | 15.98 | Score 20: | DB 10: | 241 | PVLVFMVMDLVLYLHHGH 260 | 100.08; Pred. No. 4.43e-34; |
| 2 | P94013 | P94013 | 12.7 | Best Local Similarity 100.08; | Pred. No. 4.43e-34; | 107 | PVLVFMVMDLVLYLHHGH 126 | Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |

Query Match 15.98; Score 20; DB 10; Length 381;
Best Local Similarity 100.08; Pred. No. 4.43e-34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT ID AC ID Score Query Match Length DB ID Description Pred. No.

1 P94013 P94013 15.98 Score 20: DB 10: Length 381; Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2 P94013 P94013 12.7 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

3 P94013 P94013 11.9 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 P94013 P94013 10.3 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 P94013 P94013 7.9 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

8 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

9 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

10 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

14 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

17 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

18 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

20 P94013 P94013 7.1 Best Local Similarity 100.08; Pred. No. 4.43e-34; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RX MEDLINE; 96416425.
 RA HANADA T., NISHIOCHI T., KODAMA H., NISHIMURA M., IBA K.;
 RT "CDNA cloning of a wounding-inducible gene encoding a plastid omega-3
 fatty acid desaturase from tobacco";
 RL PLANT CELL PHYSIOL. 37:606-611(1996).
 DR EMBL; D79979; D1012141; -.
 DR PFAM; PF00487; FA_desaturase; 1.
 DR MENDEL; 9312; NICTA;1208;2.
 SQ SEQUENCE 441 AA; 50310 MM; 255F96A6 CRC32;

Query Match 12.7%; Score 16; DB 10; Length 441;
 Best Local Similarity 100.0%; Pred. No. 6,47e-23;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 311 FVMMDLVLYLHHGH 326
 |||||||||||||||
 QY 111 FVMMDLVLYLHHGH 126

RESULT 3
 ID 065792 PRELIMINARY; PRT; 383 AA.
 AC 065792;
 DT 01-AUG-1998 (TREMBLREL. 07, CREATED)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE.
 GN TAFAD3.
 OS TRITICUM AESTIVUM (WHEAT).
 OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
 CC POACEAE; TRITICUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, CHIHOKU; TISSUE=LEAF, AND ROOT;
 RA HORIGUCHI G., KAKAKAMI N., KUSUMI K., KODAMA H., IBA K.;
 RL PLANT CELL PHYSIOL. 39:540-544(1998).
 DR EMBL; D84678; D1029298; -.
 SQ SEQUENCE 383 AA; 43687 MM; 50D38F40 CRC32;

Query Match 11.9%; Score 15; DB 10; Length 383;
 Best Local Similarity 100.0%; Pred. No. 3,26e-20;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 248 VMMDLVLYLHHGH 262
 |||||||||||||||
 QY 112 VMMDLVLYLHHGH 126

RESULT 4
 ID 004807 PRELIMINARY; PRT; 438 AA.
 AC 004807;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE OMEGA-3 FATTY ACID DESATURASE.
 OS PERILLA FRUTESCENS.
 CC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
 CC ASTERIDAE; GENTIANACEAE; LAMIALES; LAMIACEAE; PERILLA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OKDONG;
 RA LEE S.K., KIM K.H., KIM Y.M., HWANG Y.S.;
 RL SUBMITTED (MAY-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL; U59477; G1754795; -.
 DR PFAM; PF00487; FA_desaturase; 1.
 DR MENDEL; 16268; PERI;1208;mm16268.
 SQ SEQUENCE 438 AA; 50160 MM; EE726819 CRC32;

Query Match 10.3%; Score 13; DB 10; Length 438;
 Best Local Similarity 100.0%; Pred. No. 6,00e-15;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 WLDLVLYLHHGH 327
 |||||||||||||||
 QY 114 WLDLVLYLHHGH 126

RESULT 5
 ID 007872 PRELIMINARY; PRT; 350 AA.
 AC 007872;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE OMEGA-3 DESATURASE.
 GN DESB.
 OS SYNECHOCOCUS PCC7002.
 CC BACTERIA; CYANOBACTERIA; CHROCOCCALES; SYNECHOCOCUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97260123.
 RA SAKAMOTO T., BRYANT D.A.;
 RT "Temperature-regulated mRNA accumulation and stabilization for fatty
 acid desaturase genes in the cyanobacterium Synechococcus sp. strain
 PCC 7002";
 RL MOL. MICROBIOL. 23:1281-1292(1997).
 DR EMBL; U36389; G2197199; -.
 DR PFAM; PF00487; FA_desaturase; 1.
 SQ SEQUENCE 350 AA; 40562 MM; 969CAD61 CRC32;

Query Match 7.9%; Score 10; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1,58e-07;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 238 WLDLVLYLHH 247
 |||||||||||
 QY 114 WLDLVLYLHH 123

RESULT 6
 ID 023802 PRELIMINARY; PRT; 380 AA.
 AC 023802;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE PLASTID OMEGA-3 FATTY ACID DESATURASE (FRAGMENT).
 GN TAFAD7.
 OS TRITICUM AESTIVUM (WHEAT).
 CC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
 CC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
 CC POACEAE; TRITICUM.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, CHIHOKU; TISSUE=LEAF;
 RA HORIGUCHI G., IWAKAWA H., KODAMA H., KAKAKAMI N., NISHIMURA M.,
 RA IBA K.;
 RL PHYSIOL. PLANTARUM 96:275-283(1996).
 DR EMBL; D43688; D1008371; -.
 DR PFAM; PF00487; FA_desaturase; 1.
 FT NON TER 1
 SQ SEQUENCE 380 AA; 42633 MM; 2123FF56 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 380;
 Best Local Similarity 100.0%; Pred. No. 3,12e-05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 255 VTYLHHGH 263
 |||||||||
 QY 118 VTYLHHGH 126

RESULT 7
 ID 024626 PRELIMINARY; PRT; 398 AA.
 AC 024626;
 DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
 DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE (FRAGMENT).
GN FAD8.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM AND HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
DR EMBL: D84409; D1023307; -;
DR EMBL: D63953; D1023305; -;
DR PFAM: PF00487; FA_desaturase; 1.
FT NON_TER 1
SQ SEQUENCE 398 AA; 44789 MW; 70565SEC CRC32;

Query Match 7.1%; Score 9; DB 10; Length 398;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 272 VTYLHHGH 280
QY 118 VTYLHHGH 126
|||||

RESULT 8
ID 064907 PRELIMINARY; PRT; 407 AA.
AC 064907;
DT 01-AUG-1998 (TREMREL. 07, CREATED)
DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMREL. 07, LAST SEQUENCE UPDATE)
DE OMEGA-3 DESATURASE (FRAGMENT).
GN PXH-15.
OS PELARGONIUM X HORTORUM.
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC GERANIACEAE; PELARGONIACEAE; PELARGONIUM.
RN (1)
RP SEQUENCE FROM N.A.
RA SCHULTZ D.J., MUMMA R.O., COX-FOSTER D., CRAIG R., MEDFORD J.I.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF020204; G3133289; -;
FT NON_TER 1
SQ SEQUENCE 407 AA; 47169 MW; BC150974 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 279 VTYLHHGH 287
QY 118 VTYLHHGH 126
|||||

RESULT 9
ID 082068 PRELIMINARY; PRT; 431 AA.
AC 082068;
DT 01-NOV-1998 (TREMREL. 08, CREATED)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST SEQUENCE UPDATE)
DE W-3 DESATURASE.
OS SOLANUM TUBEROSUM (POTATO).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; SOLANACEAE; SOLANALES; SOLANACEAE; SOLANUM.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA LEON J.;
RL SUBMITTED (AUG-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN-CV. DESIREE;
RA MARTIN M.;
RL SUBMITTED (SEP-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: A0007739; E1316202; -;
SQ SEQUENCE 431 AA; 49253 MW; BAF9CD CRC32;

Query Match 7.1%; Score 9; DB 10; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 308 VTYLHHGH 316
QY 118 VTYLHHGH 126
|||||

RESULT 10
ID P93452 PRELIMINARY; PRT; 438 AA.
AC P93452;
DT 01-MAY-1997 (TREMREL. 03, CREATED)
DT 01-MAY-1997 (TREMREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMREL. 09, LAST ANNOTATION UPDATE)
DE OMEGA-3 FATTY ACID DESATURASE.
OS PETROSELINUM CRISPUM (PARSLEY) (PETROSELINUM HORTENSE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC ASTERIDAE; ARALIALES; APIACEAE; PETROSELINUM.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 97203190.
RA KIRSCH C., TAKAMIYA-WIK M., REINOLD S., HAHLEBROCK K., SOMSSICH I.E.;
RT "Rapid, transient, and highly localized induction of plasmidial
RT omega-3 fatty acid desaturase mRNA at fungal infection sites in
RT Petroselinum crispum."
RL PROC. NATL. ACAD. SCI. U.S.A. 94:2079-2084(1997).
DR EMBL: U75745; G1786066; -;
DR PFAM: PF00487; FA_desaturase; 1.
DR MENDEL: 9768; Petcr; 1208; 1
SQ SEQUENCE 438 AA; 50391 MW; 9E77A228 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 438;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 315 VTYLHHGH 323
QY 118 VTYLHHGH 126
|||||

RESULT 11
ID 023824 PRELIMINARY; PRT; 443 AA.
AC 023824;
DT 01-JAN-1998 (TREMREL. 05, CREATED)
DT 01-JAN-1998 (TREMREL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMREL. 08, LAST ANNOTATION UPDATE)
DE FATTY ACID DESATURASE.
GN FAD7.
OS ZEA MAYS (MAIZE).
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC EUPHYLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC POACEAE; ZEA.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-HONEY BANTUM;
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RL PLANT MOL. BIOL. 0:0-0(1997).
RN [2]
RP SEQUENCE OF 182-443 FROM N.A.
RC STRAIN-HONEY BANTUM;
RX MEDLINE: 98145435.
RA BERBERICH T., HARADA M., SUGAMARA K., KODAMA H., IBA K., KUSANO T.;
RT "Two maize genes encoding omega-3 fatty acid desaturase and their
RT differential expression to temperature."
RN [2]

RL PLANT MOL. BIOL. 36:297-306(1998).
DR EMBL: D63954; D1023306; -.
DR EMBL: D63952; D1023304; -.
DR PFAM: PF00487; FA_desaturase; 1.
SQ SEQUENCE 443 AA; 49437 MW; E8BC6757 CRC32;

Query Match 7.1%; Score 9; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 3.12e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 317 VTYLHHGH 325
|||||
QY 118 VTYLHHGH 126

RESULT 12
ID 027483 PRELIMINARY; PRT; 254 AA.
AC 027483;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 28.3 KD PROTEIN.
GN MTH1434.
OS METHANOBACTERIUM THERMAUTOTROPHICUM.
OC ARCHAEA; EURYARCHAEOTA; METHANOBACTERIALES; METHANOBACTERIACEAE;
OC METHANOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H:
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDREGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CAROSO A., BUSH D., SAFER H., PATWEL D., PRABHAKAR S.,
RA MCDONALD L., SHIMER G., GOVAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT delah: functional analysis and comparative genomics.";
RL J. BACTERIOL. 179:7135-7155(1997).
DR EMBL: AE000905; G2622546; -.
KW HYPOTHEICAL PROTEIN.
SQ SEQUENCE 254 AA; 28253 MW; AA8DF6C5 CRC32;

Query Match 5.6%; Score 7; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 220 YGIPYLV 226
|||||
QY 104 YGIPYLV 110

RESULT 13
ID 063255 PRELIMINARY; PRT; 255 AA.
AC 063255;
DT 01-NOV-1998 (TREMBLREL. 08, CREATED)
DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE COBALT ABC TRANSPORTER, ATP-BINDING PROTEIN.
GN T70227.
OS TREPONEMA PALLIDUM.
OC BACTERIA; SPIROCHAETALES; SPIROCHAETACEAE; TREPONEMA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98332770.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTINACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;

RT "Complete Genome Sequence of Treponema pallidum, the Syphilis
RT Spirochete.";
RL SCIENCE 281:375-388(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
RA DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
RA SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
RA KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
RA MCDONALD L., ARTINACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
RA HATCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
RA VENTER J.C.;
RL SUBMITTED (MAR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AE001204; G3322495; -.
DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
KW ATP-BINDING; TRANSPORT.
SQ SEQUENCE 255 AA; 27321 MW; 81400AE7 CRC32;

Query Match 5.6%; Score 7; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 104 CARGPLQ 110
|||||
QY 93 CARGPLQ 99

RESULT 14
ID 005589 PRELIMINARY; PRT; 419 AA.
AC 005589;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE HYPOTHEICAL 38.8 KD PROTEIN.
GN RV1004C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIACEAE;
OC ACTINOMYCETALES; CORYNEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE: 98295887.
RA COLE S.T., BROSCHE R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D.,
RA GORDON S.V., EIGLMAYER K., GAS S., BARRY III C.E., TEKAIA F.,
RA BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
RA DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
RA HORNSEY T., JAGELS K., KROGH A., MCLEAN J., MOUE S., MURPHY L.,
RA OLIVER S., OSBORNE J., O'VAIL M.A., RAJANDREAM M.A., ROGERS J.,
RA RUTTER S., SEEGER K., SKELTON S., SQUARDS S., SOARDS R., SULSTON J.E.,
RA TAYLOR K., WHITEHEAD S., BARRELL B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL NATURE 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA PARKHILL J.;
RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: Z94752; E1299781; -.
KW HYPOTHEICAL PROTEIN.
SQ SEQUENCE 419 AA; 38785 MW; 4B1AD82D CRC32;

Query Match 5.6%; Score 7; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 4.90e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 ASLAMA 260
|||||
QY 86 ASLAMA 92

RESULT 15
ID 040118 PRELIMINARY; PRT; 436 AA.

AC 040118;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE DELTA-15 LINEOYL DESATURASE.
 OS LIMNANTHES DOUGLASSII.
 OC EUKARYOTA; VIRIDIPHYTES; STREPTOPHYTES; EMBRYOPHYTES; TRACHEOPHYTES;
 OC EUPHYLOPHYTES; SPERMATOPHYTES; MAGNOLIOPHYTES; EUDICOTYLEDONS; ROSIDAE;
 OC CAPPALES; LIMNANTHACEAE; LIMNANTHES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95334518.
 RA BHELIA R.S.; MACKENZIE S.L.;
 RT "Nucleotide sequence of a cDNA from Limnantes douglasii L. encoding
 a delta-15 linoleic acid desaturase.";
 RL PLANT PHYSIOL. 108:861-861(1995).
 DR EMBL; U17063; G699390.
 DR PFM; PF00487; FA_desaturase; 1.
 DR MENDEL; 8699; LINDO; 1208; 1.
 SO SEQUENCE 436 AA; 50093 MW; 327D77FE CRC32;

Query Match 5.6%; Score 7; DB 10; Length 436;
 Best Local Similarity 100.0%; Pred. No. 4.90e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 194 HHONHGH 200

QY 1 HHONHGH 7

Search completed: Sat Aug 21 12:52:57 1999
 Job time : 42 secs.

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 W O R L D
 ***** (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:49:24 1999; Maspar time 6.93 Seconds

Tabular output not generated. 386.472 Million cell updates/sec

Title: >US-09-219-935-15

Description: (1-126) from US09219935.pep

Sequence: 1 HHQNHGHRDESMHPIREK.....PVLVFMVMDLVYLIHHGH 126

Scoring table: TABLE uniprottable

Gap 60

Searched: 170751 seqs, 2126608 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

a:geneseqs

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 2.519; Variance 0.623; scale 4.044

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|----|-------------|-----------------------|
| 1 | 126 | 100.0 | 126 | 7 | R37597 | Sequence of an intern |
| 2 | 16 | 12.7 | 453 | 7 | R37596 | Sequence of soybean p |
| 3 | 10 | 7.9 | 447 | 24 | W13361 | Sesame omega-3 alipha |
| 4 | 9 | 7.1 | 378 | 7 | R37591 | Sequence of microsoma |
| 5 | 9 | 7.1 | 380 | 7 | R37595 | Sequence of microsoma |
| 6 | 9 | 7.1 | 383 | 11 | R60498 | Linoleic-acid-desatur |
| 7 | 9 | 7.1 | 386 | 7 | R37592 | Sequence of delta-15 |
| 8 | 9 | 7.1 | 404 | 7 | R37594 | Sequence of plastid d |
| 9 | 9 | 7.1 | 435 | 11 | R60500 | Linoleic-acid-desatur |
| 10 | 9 | 7.1 | 446 | 11 | R60499 | Linoleic-acid-desatur |
| 11 | 9 | 7.1 | 446 | 7 | R37593 | Sequence of a plastid |
| 12 | 7 | 5.6 | 156 | 7 | R37598 | Sequence of a plastid |
| 13 | 7 | 5.6 | 447 | 2 | P70314 | Sequence of flagellin |
| 14 | 6 | 4.8 | 68 | 29 | W55401 | H. pylori ORF hp4p113 |
| 15 | 6 | 4.8 | 131 | 22 | W20697 | H. pylori putative tr |
| 16 | 6 | 4.8 | 160 | 5 | R27885 | Pheromone receptor cl |

| Result ID | Score | Query Match | Length | ID | Description | Pred. No. |
|-----------|-------|-------------|--------|----|-------------|-------------------------|
| 17 | 6 | 4.8 | 168 | 21 | W20521 | Helicobacter pylori c |
| 18 | 6 | 4.8 | 170 | 29 | W44794 | B. afzelii strain B02 |
| 19 | 6 | 4.8 | 197 | 31 | W59156 | H. influenza rhnb pro |
| 20 | 6 | 4.8 | 260 | 28 | W36115 | Yeast ribosomal prote |
| 21 | 6 | 4.8 | 301 | 22 | W20732 | H. pylori cell envelope |
| 22 | 6 | 4.8 | 318 | 25 | W32065 | Human beta-sarcoglyca |
| 23 | 6 | 4.8 | 318 | 25 | W32064 | Human beta-sarcoglyca |
| 24 | 6 | 4.8 | 318 | 25 | W32060 | H. sapiens beta-sarco |
| 25 | 6 | 4.8 | 318 | 25 | W32066 | Human beta-sarcoglyca |
| 26 | 6 | 4.8 | 322 | 5 | R26063 | Encodes rat CRF-bind |
| 27 | 6 | 4.8 | 322 | 29 | W52177 | Human CRF-binding pro |
| 28 | 6 | 4.8 | 322 | 29 | W52178 | Rat CRF-binding prote |
| 29 | 6 | 4.8 | 324 | 20 | W11860 | Human proteosome subu |
| 30 | 6 | 4.8 | 324 | 13 | R74000 | Full length ovine CRF |
| 31 | 6 | 4.8 | 342 | 26 | W26671 | Mouse alpha-fucosyltr |
| 32 | 6 | 4.8 | 342 | 21 | W11820 | Murine myeloid-lineag |
| 33 | 6 | 4.8 | 356 | 26 | W26676 | Borrelia variabile maj |
| 34 | 6 | 4.8 | 361 | 4 | R20816 | Human epithelial CD44 |
| 35 | 6 | 4.8 | 361 | 18 | R91444 | Human haematopoietic |
| 36 | 6 | 4.8 | 362 | 1 | R07355 | B7 adhesion receptor. |
| 37 | 6 | 4.8 | 454 | 18 | R97842 | Kaposi's sarcoma asso |
| 38 | 6 | 4.8 | 454 | 17 | R93616 | Kaposi's sarcoma asso |
| 39 | 6 | 4.8 | 493 | 17 | R91445 | Human epithelial CD44 |
| 40 | 6 | 4.8 | 493 | 4 | R20817 | Epithelial CD44 Antig |
| 41 | 6 | 4.8 | 653 | 7 | R37425 | IDUA. |
| 42 | 6 | 4.8 | 680 | 2 | R07453 | First open reading fr |
| 43 | 6 | 4.8 | 680 | 30 | W45516 | Saccharomyces cerevis |
| 44 | 6 | 4.8 | 719 | 38 | W82644 | Enfilonia sp. extende |
| 45 | 6 | 4.8 | 1275 | 39 | W82594 | H. contortus PGP-A pr |

ALIGNMENTS

RESULT 1
 ID R37597 standard: Protein: 126 AA.
 AC R37597;
 DT 01-OCT-1993 (first entry)
 DE Sequence of an internal region of a corn seed delta-15
 DE desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Zea mays, clone pPCR20.
 PN W09311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; U10284.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E. I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: Q43209.
 PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure: Page 152-153; 167pp; English.
 CC PCR3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the PCR3
 CC insert was also used. The identity of the expression product of PCR3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q43224. Q43209 is the
 CC complete nucleotide sequence of a 396 bp polymerase chain reaction
 CC product derived from corn seed mRNA that is found in the insert of
 CC plasmid pPCR20. Nucleotides 1 to 31 and 364 to 396 correspond to
 CC the amplification primers described in Q43221 and Q43222
 CC respectively. Nucleotides 31 to 365 encode a region that is 61.98
 CC identical to the region between amino acids 137 and 249 of R37591.
 SQ Sequence 126 AA;

Query Match 100.0%; Score 126; DB 7; Length 126;

Db 251 vtylhhgh 259
 |||||||
 QY 118 VTYLHHGH 126

RESULT 5
 ID R37595 standard; Protein; 380 AA.

AC R37595;
 DT 01-OCT-1993 (first entry)
 DE Sequence of microsomal delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Glycine max, clone pXf1.
 PN MO9311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; US-804259.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: 043207.

PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure: Page 144-146; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the PCF3
 CC insert was also used. The identity of the expression product of PCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q4324. Arabidopsis delta-15
 CC desaturase cDNA was used as a hybridization probe to isolate a
 CC glycerolipid desaturase cDNA from soybean. Plasmid pXf1 was
 CC deposited under ATCC 68874.
 SO Sequence 380 AA;

Query Match 7.1%; Score 9; DB 7; Length 380;
 Best Local Similarity 100.0%; Pred. No. 1.40e-02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 256 vtylhhgh 264
 |||||||
 QY 118 VTYLHHGH 126

RESULT 6
 ID R60498 standard; Protein; 383 AA.

AC R60498;
 DT 28-MAR-1995 (first entry)
 DE Linoleic-acid-desaturase: fad3.
 KW Linoleic-acid-desaturase; fad3; oilseed rape; rapeseed;
 KM transgenic plant; crop improvement; yeast artificial chromosome;
 KM YAC; linolenic acid.
 OS Brassica napus.
 PN MO9418337-A.
 PD 18-AUG-1994.
 PE 04-FEB-1994; US-014321.
 PR 05-FEB-1993; US-014431.
 PR 22-NOV-1993; US-156551.
 PA (MONS) MONSANTO CO.
 PA (UNMS) UNIV MICHIGAN STATE.
 PI Aronoff VJA, Gibson SI, Kishore GM, Ruff TG, Somerville CR;
 DR WPI: 94-279758/34.
 DR N-PSDB: 071203.

PT Genetically transformed plants with altered linolenic acid
 PT content - contg recombinant, double-stranded DNA encoding
 PT linoleic acid desaturase, or the antisense of the coding
 PT sequence

PS Disclosure; Page 69-71; 144pp; English.
 CC cDNA encoding the linoleic-acid-desaturase (fad3) of B. napus was
 CC isolated from a YAC library using RFLP 220 and ASA2 markers as
 CC probes. Isolated DNA was amplified using the primers given in
 CC Q71204-09, and used to screen YAC libraries. The fad3 gene was
 CC identified in YAC EW/D11.
 SQ Sequence 383 AA;

Query Match 7.1%; Score 9; DB 11; Length 383;
 Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 254 vtylhhgh 262
 |||||||
 QY 118 VTYLHHGH 126

RESULT 7
 ID R37592 standard; Protein; 386 AA.

AC R37592;
 DT 01-OCT-1993 (first entry)
 DE Sequence of delta-15 desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Arabidopsis thaliana, clone PCF3.
 PN MO9311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; US-804259.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.
 DR N-PSDB: 043202.

PT Isolated nucleic acid fragment, for plant lipid compsn.
 PT modification - comprises nucleic acid sequence encoding fatty
 acid desaturase or related enzyme with high aminoacid identity to
 PT specific polypeptide
 PS Disclosure: Page 127-129; 167pp; English.
 CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
 CC fragment containing wild-type genomic DNA as a radiolabeled
 CC hybridization probe. One of the sequencing primers made to the PCF3
 CC insert was also used. The identity of the expression product of PCF3
 CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
 CC its biological overexpression in plant tissues. Conserved regions of
 CC R37592 are useful in designing long oligomers for hybridization as
 CC well as shorter ones for use as primers in the PCR. The sequences
 CC of useful regions are given in Q43213-Q4324.
 SO Sequence 386 AA;

Query Match 7.1%; Score 9; DB 7; Length 386;
 Best Local Similarity 100.0%; Pred. No. 1.40e-02;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 257 vtylhhgh 265
 |||||||
 QY 118 VTYLHHGH 126

RESULT 8
 ID R37594 standard; Protein; 404 AA.

AC R37594;
 DT 01-OCT-1993 (first entry)
 DE Sequence of plastid delta-15 glycerolipid desaturase.
 KW Lipid composition; modification; fatty acid desaturase; enzyme.
 OS Brassica napus, clone pBNSfd-2.
 PN MO9311245-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; US-804259.
 PR 04-DEC-1991; US-804259.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
 PI Yadav NS;
 DR WPI: 93-197063/24.

DR N-PSDB: 043206.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 140-141; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the PCF3
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. The cDNA inserts
CC from PCF3 and PCM2 were used to isolate PBNSF3-2. Plasmid PBNSF3-2
CC was deposited as ATCC No. 68854. PBNSF3-3 (043206) corresp. to a
CC novel Brassica napus seed desaturase different from that shown in
CC 043205.
SQ Sequence 404 AA;

Query Match 7.1%; Score 9; DB 7; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 277 vtylhhgh 285
|||
OY 118 VTYLHHGH 126

RESULT 9
ID R60500 standard; protein; 435 AA.
AC R60500: 28-MAR-1995 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Linoleic-acid-desaturase; fad; transgenic plant; crop improvement;
KW Linoleic acid.
OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Arondei VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: 071211.
PT Genetically transformed plants with altered linoleic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 79-81; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of linoleic-
CC acid-desaturase fad of Arabidopsis are provided.
SQ Sequence 435 AA;

Query Match 7.1%; Score 9; DB 11; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 312 vtylhhgh 320
|||
OY 118 VTYLHHGH 126

RESULT 10
ID R60499 standard; protein; 446 AA.
AC R60499: 28-MAR-1995 (first entry)
DE Linoleic-acid-desaturase fad.
KW Linoleic-acid-desaturase; fad; transgenic plant; crop improvement;
KW Linoleic acid.

OS Arabidopsis.
PN W09418337-A.
PD 18-AUG-1994.
PF 04-FEB-1994; U01321.
PR 05-FEB-1993; US-014431.
PR 22-NOV-1993; US-156551.
PA (MONS) MONSANTO CO.
PA (UNMS) UNIV MICHIGAN STATE.
PI Arondei VJA, Gibson ST, Kishore GM, Ruff TG, Somerville CR;
DR WPI: 94-279758/34.
DR N-PSDB: 071210.
PT Genetically transformed plants with altered linoleic acid
PT content - contg recombinant, double-stranded DNA encoding
PT linoleic acid desaturase, or the antisense of the coding
PT sequence
PS Disclosure: Page 75-77; 144p; English.
CC The cDNA sequence and deduced amino acid sequence of linoleic-
CC acid-desaturase fad of Arabidopsis are provided.
SQ Sequence 446 AA;

Query Match 7.1%; Score 9; DB 11; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 319 vtylhhgh 327
|||
OY 118 VTYLHHGH 126

RESULT 11
ID R37593 standard; protein; 446 AA.
AC R37593: 01-OCT-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid desaturase.
KW Lipid composition; modification; fatty acid desaturase; enzyme.
OS Arabidopsis thaliana, clone PACR2-2.
PN W09311245-A.
PD 10-JUN-1993.
PF 03-DEC-1992; U10284.
PR 04-DEC-1991; US-804259.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Browne J, Grau LP, Kinney AJ, Pierce JW, Wierzbicki AM,
PI Yadav NS;
DR WPI: 93-197063/24.
DR N-PSDB: 043204.
PT Isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure: Page 132-134; 167pp; English.
CC PCF3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the
CC insert was also used. The identity of the expression product of PCF3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in 043213-043224. In contrast to the
CC constitutive expression of the gene encoding (R37592), the mRNA
CC corresponding to 043204 is abundant in green tissues, rare in roots
CC and leaves, and is about three-fold more abundant in leaf than that
CC of 043202. R37592 and R37593 show overall homology of approx.
CC 80%.
SQ Sequence 446 AA;

Query Match 7.1%; Score 9; DB 7; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.40e-02;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 319 vtylhhgh 327
|||
OY 118 VTYLHHGH 126

| | |
|--------|-----------------------------------|
| RESULT | 12 |
| ID | R37598 standard; Protein; 156 AA. |

DT 01-Oct-1993 (first entry)
DE Sequence of a plastid delta-15 fatty acid.
KW Lipid composition; modification; fatty acid desaturase; enzyme
OS Arabidopsis thaliana, clone pFedr-2 and pYcp7.
ID 10000112

PT isolated nucleic acid fragment, for plant lipid compsn.
PT modification - comprises nucleic acid sequence encoding fatty
PT acid desaturase or related enzyme with high aminoacid identity to
PT specific polypeptide
PS Disclosure; Page 155; 167pp; English.
CC pPCR3 was isolated from a cDNA library using a 5.2 kb Hind III
CC fragment containing wild-type genomic DNA as a radiolabeled
CC hybridization probe. One of the sequencing primers made to the pPCR3
CC insert was also used. The identity of the expression product of pPCR3
CC as the Arabidopsis microsomal delta-15 desaturase was confirmed by
CC its biological overexpression in plant tissues. Conserved regions of
CC R37592 are useful in designing long oligomers for hybridization as
CC well as shorter ones for use as primers in the PCR. The sequences
CC of useful regions are given in Q43213-Q43224. Q43210 is the partial
CC composite sequence derived from the inserts in plasmids pRdx-2 and
CC pRdx7. R37598 is a deduced partial peptide sequence of its ORF.
Q4 Sequence 156 AA;

| | | | | |
|-----------------------|---------|---------------------|-----------|---------------|
| Query Match | 5.68; | Score 7; | DB 7; | Length 156; |
| Best Local Similarity | 100.0%; | Pred. No. 4.96e+00; | | |
| Matches | 7; | Conservative | 0; | Mismatches 0; |
| | | | Indels 0; | Gaps 0 |

```
Db 147 hhqnhgh 1
    1111111
QY 1 HHQNHGH 7
```

| | |
|--------|-----------------------------------|
| RESULT | 13 |
| ID | P70314 standard; Protein; 447 AA. |

DT 06-JUN-1991 (first entry)
DE Sequence of flagellin deletion mutant encoded by *Escherichia coli*
DE K-12 KH552 haq gene in pFD313.
KW Secretion vector; secretion system; flagella.
KW *Escherichia coli*.

PT DNA encoding flagellin - used or fusing to foreign DNA for
PT excision of peptide(s), determ. of epitope(s) and prepn. of
PT antigens
PS Example: Fla 15b, 119pp; English.
CC The hag gene encoding flagellin is inserted into a vector and then
CC the hag gene is cut or partially deleted and linker DNA inserted.
CC DNA coding for a foreign peptide is inserted into the linker DNA and
CC the vector introduced into a bacterium. As a result, the foreign
CC peptide is excrated from the bacterium as a peptide is fused with
CC flagellin. Under certain conditions the excrated peptide forms

CC flagella, thus facilitating the recovery of the peptide. The examples
CC prepare vectors contg. the hag gene (N70495) from which the sequence
CC between bp 583 to 1143 has been deleted (see N70496, N70497, N70500,
CC N70501, N70502, N70503, N70504).
50 Sequence 447 AA:

| | | | | |
|-----------------------|---------|---------------------|-------|--------------------------------|
| Query Match | 5.68; | Score 7; | DB 2; | Length 447; |
| Best Local Similarity | 100.08; | Pred. No. 4.96e+00; | | |
| Matches | 7; | Conservative | 0; | Mismatches 0; Indels 0; Gaps 0 |

| | | | |
|----|-----|---------|-----|
| Db | 245 | yrspgk1 | 251 |
| | | | |
| QY | 49 | YRSPGKL | 55 |

| | |
|--------|----------------------------------|
| RESULT | 14 |
| ID | W55401 standard; Protein; 68 AA. |
| NC | REF401 |

DT 18-JUN-1998 (first entry)
DE H. pylori ORF hp04135orf5 protein.
KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
KW identification; binding compound; bacteria; life cycle; activator
KW inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
OS Helicobacter pylori.
NN W09737044-A1.

PT Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection
 PT Claim 14; Page 615; 1145pp. English.

CC This sequence is a *H. pylori* protein of unspecified function.
CC The protein may be used in a vaccine to prevent or treat *H. pylori*
CC infection or to identify *H. pylori* polypeptide binding compounds.
CC useful as potential *H. pylori* life cycle activators or inhibitors. The
CC DNA and probes derived from it may be used for the identification of
CC *H. pylori* in a sample and the diagnosis of *H. pylori* infection. Nucleic
CC acid sequences complementary to the DNA act as antisense sequences and
CC can be used to prevent the translation of *H. pylori* mRNA. Antibodies
CC against the protein can be used in immunoassays to evaluate the abundance
CC and distribution of *H. pylori*-specific antigens. The genomic sequence of
CC *H. pylori* (ATCC 55679) was determined from overlapping contigs generated
CC by mechanically shearing the bacterial DNA. The sequences were analysed
CC for ORF of at least 180 nucleotides, and the predicted coding regions
CC defined by computer evaluation. No identify likely *H. pylori* antigens for
CC vaccine development, the amino acid sequences predicted from various ORF
CC were analysed for significant homology to other known or exported
CC membrane proteins. Having identified and determined the sequences of
CC interest, particular regions can be isolated from *H. pylori* by PCR
CC amplification for recombinant polypeptide production, e.g. in *E. coli*
CC hosts.

| | | | | |
|-----------------------|---------|---------------------|--------|--------------------------------|
| Query Match | 4.88; | Score 6; | DB 29; | Length 68; |
| Best Local Similarity | 100.0%; | Pred. No. 7.37e+01; | | |
| Matches | 6; | Conservative | 0; | Mismatches 0; Indels 0; Gaps 0 |

| | | | |
|----|----|--------|-----|
| Db | 32 | qvlkmy | 37 |
| | | | |
| QY | 99 | QVLKMY | 104 |

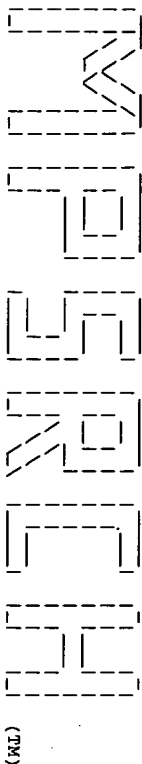
RESULT 15
ID W20697 standard; Protein; 131 AA.

AC W20697;
 DT 15-JUL-1997 (first entry)
 DE H. pylori putative transmembrane protein 05ae20220orf51.
 KW Vaccine; prevention; treatment; infection; identification;
 KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
 KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope;
 KW transmembrane; membrane spanning region.
 OS Helicobacter pylori.
 PN WO9640893-A1.
 PD 19-DEC-1996.
 PE 06-JUN-1996; U09122.
 PR 07-JUN-1995; US-487032.
 PR 01-APR-1996; US-630405.
 PA (ASTR) ASTRA AB.
 PI Berglindh OT, Smith D, Mellgaard BL;
 DR WPI; 97-052306/05.
 DR N-PSDB; T67950.
 PT Helicobacter pylori nucleic acid sequences and related
 PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
 PT infection, and to detect Helicobacter
 PS Claim 73; Page 1116; 1481pp; English.
 CC The present sequence represents a Helicobacter pylori protein likely
 CC to contain a single membrane spanning region.
 CC The protein may be used in a vaccine to prevent or treat H. pylori
 CC infection or to identify H. pylori polypeptide binding compounds,
 CC useful as potential H. pylori life cycle activators or inhibitors.
 CC The genomic sequence of H. pylori (ATCC 55679) was determined from
 CC overlapping contigs generated by mechanically shearing the bacterial
 CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
 CC and the predicted coding regions defined by computer evaluation. To
 CC identify likely H. pylori antigens for vaccine development, the amino
 CC acid sequences predicted from various ORF were analysed for significant
 CC homology to other known or exported membrane proteins. Having identified
 CC and determined the sequences of interest, particular regions can be
 CC isolated from H. pylori by PCR amplification for recombinant polypeptide
 CC production, e.g. in E. coli hosts.
 SQ Sequence 131 AA;

Query Match 4.88; Score 6; DB 22; Length 131;
 Best Local Similarity 100.0%; Pred. No. 7.37e+01;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 50 seqs 55
 |||||
 QY 62 SSDLFS 67

Search completed: Sat Aug 21 12:50:44 1999
 Job time : 80 secs.



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MPerch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Sat Aug 21 12:53:14 1999; Maspar time 2.46 Seconds
Tabular output not generated. 518.993 Million cell updates/sec

Title: >US-09-219-935-15
Description: (1-126) from US09219935.pep
Perfect Score: 126
Sequence: 1 HHQNHGHIHDESMHPIEK.....FLVFMVMDLVLYLHHGH 126

Scoring table: TABLE uniprottable
Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCR9_COMB 4:Backfiles1

Statistics: Mean 2.379; Variance 0.615; scale 3.866

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
|------------|-------|-------------|--------|------------|------------------------|-----------|
| 1 | 126 | 100.0 | 126 | PCT-US92-1 | Sequence 15, Applicati | 5.11e-190 |
| 2 | 15 | 12.7 | 453 | PCT-US92-1 | Sequence 13, Applicati | 1.31e-12 |
| 3 | 9 | 7.1 | 378 | PCT-US92-1 | Sequence 7, Applicati | 7.47e-03 |
| 4 | 9 | 7.1 | 380 | PCT-US92-1 | Sequence 11, Applicati | 7.47e-03 |
| 5 | 9 | 7.1 | 383 | PCT-US94-0 | Sequence 2, Applicatio | 7.47e-03 |
| 6 | 9 | 7.1 | 386 | PCT-US92-1 | Sequence 2, Applicatio | 7.47e-03 |
| 7 | 9 | 7.1 | 404 | PCT-US92-1 | Sequence 9, Applicatio | 7.47e-03 |
| 8 | 9 | 7.1 | 435 | PCT-US94-0 | Sequence 12, Applicati | 7.47e-03 |
| 9 | 9 | 7.1 | 446 | PCT-US92-1 | Sequence 5, Applicatio | 7.47e-03 |
| 10 | 9 | 7.1 | 446 | PCT-US94-0 | Sequence 10, Applicati | 7.47e-03 |
| 11 | 7 | 5.6 | 156 | PCT-US92-1 | Sequence 17, Applicati | 2.36e+00 |
| 12 | 6 | 4.8 | 24 | US-08-320- | Sequence 20, Applicati | 3.40e+01 |
| 13 | 6 | 4.8 | 24 | US-08-320- | Sequence 14, Applicati | 3.40e+01 |
| 14 | 6 | 4.8 | 24 | US-08-314- | Sequence 20, Applicati | 3.40e+01 |
| 15 | 6 | 4.8 | 37 | US-08-320- | Sequence 8, Applicatio | 3.40e+01 |
| 16 | 6 | 4.8 | 37 | US-08-320- | Sequence 26, Applicati | 3.40e+01 |
| 17 | 6 | 4.8 | 101 | PCT-US92-1 | Sequence 40, Applicati | 3.40e+01 |
| 18 | 6 | 4.8 | 101 | US-08-190- | Sequence 2, Applicatio | 3.40e+01 |
| 19 | 6 | 4.8 | 101 | US-08-468- | Sequence 2, Applicatio | 3.40e+01 |
| 20 | 6 | 4.8 | 258 | PCT-US94-1 | Sequence 1, Applicatio | 3.40e+01 |
| 21 | 6 | 4.8 | 295 | PCT-US94-1 | Sequence 6, Applicatio | 3.40e+01 |
| 22 | 6 | 4.8 | 298 | PCT-US94-1 | Sequence 2, Applicatio | 3.40e+01 |
| 23 | 6 | 4.8 | 318 | US-08-547- | Sequence 2, Applicatio | 3.40e+01 |

| | | | | | | |
|----|---|-----|------|------------|------------------------|----------|
| 24 | 6 | 4.8 | 322 | PCT-US93-1 | Sequence 3, Applicatio | 3.40e+01 |
| 25 | 6 | 4.8 | 322 | PCT-US92-0 | Sequence 1, Applicatio | 3.40e+01 |
| 26 | 6 | 4.8 | 322 | PCT-US92-0 | Sequence 1, Applicatio | 3.40e+01 |
| 27 | 6 | 4.8 | 322 | PCT-US93-1 | Sequence 1, Applicatio | 3.40e+01 |
| 28 | 6 | 4.8 | 322 | US-08-462- | Sequence 3, Applicatio | 3.40e+01 |
| 29 | 6 | 4.8 | 322 | US-08-097- | Sequence 1, Applicatio | 3.40e+01 |
| 30 | 6 | 4.8 | 322 | US-08-097- | Sequence 3, Applicatio | 3.40e+01 |
| 31 | 6 | 4.8 | 322 | US-08-480- | Sequence 3, Applicatio | 3.40e+01 |
| 32 | 6 | 4.8 | 342 | US-08-483- | Sequence 2, Applicatio | 3.40e+01 |
| 33 | 6 | 4.8 | 361 | US-07-946- | Sequence 6, Applicatio | 3.40e+01 |
| 34 | 6 | 4.8 | 361 | US-08-478- | Sequence 6, Applicatio | 3.40e+01 |
| 35 | 6 | 4.8 | 362 | 5504194-2 | Patent No. 5504194. | 3.40e+01 |
| 36 | 6 | 4.8 | 363 | US-08-478- | Sequence 7, Applicatio | 3.40e+01 |
| 37 | 6 | 4.8 | 411 | US-07-684- | Sequence 2, Applicatio | 3.40e+01 |
| 38 | 6 | 4.8 | 430 | US-08-476- | Sequence 44, Applicati | 3.40e+01 |
| 39 | 6 | 4.8 | 430 | US-08-833- | Sequence 44, Applicati | 3.40e+01 |
| 40 | 6 | 4.8 | 454 | PCT-US95-1 | Sequence 33, Applicati | 3.40e+01 |
| 41 | 6 | 4.8 | 454 | US-08-420- | Sequence 33, Applicati | 3.40e+01 |
| 42 | 6 | 4.8 | 503 | US-08-478- | Sequence 2, Applicatio | 3.40e+01 |
| 43 | 6 | 4.8 | 503 | US-08-483- | Sequence 2, Applicatio | 3.40e+01 |
| 44 | 6 | 4.8 | 680 | US-08-674- | Sequence 2, Applicatio | 3.40e+01 |
| 45 | 6 | 4.8 | 2396 | US-08-157- | Sequence 2, Applicatio | 3.40e+01 |

ALIGNMENTS

RESULT 1 STANDARD; PRT; 126 AA.

XX PCT-US92-10284-15

XXXXXX

Sequence 15, Application PC/TUS9210284

GENERAL INFORMATION:

APPLICANT: Browne, John, Kinney, Anthony J.,

APPLICANT: Pierce, John, Wierzbicki, Anna M.,

APPLICANT: Yadav, Narendra S., Perez-Grau, Luis

TITLE OF INVENTION: Fatty Acid Desaturase Genes

TITLE OF INVENTION: from Plants

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STATE: Delaware

COUNTRY: U.S.A.

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: Macintosh System, 6.0

SOFTWARE: Microsoft Word, 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10284

FILING DATE: 19921203

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/804,259

FILING DATE: 4 DECEMBER 1991

ATTORNEY/AGENT INFORMATION:

NAME: Floyd, Linda A.

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BB-1036-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 992-4929

TELEFAX: (302) 892-7949

TELEX: 833420

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 126 amino acids

CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: YES
CC FRAGMENT TYPE: internal
CC ORIGINAL SOURCE: internal
CC ORGANISM: Zea mays
CC IMMEDIATE SOURCE:
CC CLONE: pPCR20
SQ SEQUENCE 126 AA; 14668 MW; 96232 CN;

Query Match 100.0%; Score 126; DB 3; Length 126;
Best Local Similarity 100.0%; Pred. No. 5,11e-190;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHNHGHIHDESNHPTTEKLYROLEPRTKLRFTVPPPLAFVYLLYRSFGKLSHFL 60
|||
QY 1 HHNHGHIHDESNHPTTEKLYROLEPRTKLRFTVPPPLAFVYLLYRSFGKLSHFL 60
|||
Db 61 PSSDLFSPKESDVWSTTCIMLASILAMACAFGLQVLKMGIPLYFVMMLDVTV 120
|||
QY 61 PSSDLFSPKESDVWSTTCIMLASILAMACAFGLQVLKMGIPLYFVMMLDVTV 120
|||
Db 121 LHHGH 126
|||
QY 121 LHHGH 126
|||

RESULT 2
ID PCT-US92-10284-13 STANDARD: PRT: 453 AA.
XX
AC xxxxxx
DT
DE Sequence 13, Application PC/TUS9210284
XX
CC Sequence 13, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420

CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 453 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 453 AA; 51362 MW; 1146882 CN;

Query Match 12.7%; Score 16; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 1,31e-12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 320 FVXMDLVTVLHHGH 335
|||
QY 111 FVXMDLVTVLHHGH 126
|||

RESULT 3
ID PCT-US92-10284-7 STANDARD: PRT: 378 AA.
XX
AC xxxxxx
DT
DE Sequence 7, Application PC/TUS9210284
XX
CC Sequence 7, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 378 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 378 AA; 43528 MW; 793455 CN;

Query Match 7.1%; Score 9; DB 3; Length 378;
Best Local Similarity 100.0%; Pred. No. 7,47e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: 07/804,259
CC      FILING DATE: 4 DECEMBER 1991
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Floyd, Linda A.
CC      REGISTRATION NUMBER: 33,692
CC      REFERENCE/DOCKET NUMBER: BB-1036-A
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 366 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 366 AA:44076 MW: 854247 CN:

```

| | | | | |
|-----------------------|---------|---------------------|-----------|---------------|
| Query Match | 7.1% | Score 9; | DB 3; | Length 366; |
| Best Local Similarity | 100.0%; | Pred. No. 7.47e-03; | | |
| Matches | 9; | Conservative | 0; | Mismatches 0; |
| | | | Indels 0; | Gaps 0; |

| | | | |
|----|-----|----------|-----|
| Db | 257 | VTYLNHGH | 265 |
| | | | |
| QY | 118 | VTYLNHGH | 126 |

| RESULT | 7 | STANDARD; | PRT; | 404 AA. |
|--------|------------------|-----------|------|---------|
| ID | PCT-US92-10284-9 | | | |

AC XXXXXXXX

| | |
|----|---------------------------------------|
| DE | Sequence 9, Application PC/TUS9210284 |
| XX | |
| CC | Sequence 9, Application PC/TUS9210284 |

CC
CC
CC
CC
CC
CC
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CC
CC
CC

APPLICANT: Browsey, John, Kinney, Anthony J.,
APPLICANT: Pierce, John, Wierzbicki, Anna M.,
APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
TITLE OF INVENTION: Fatty Acid Desaturase Genes
FROM PLANTS
NUMBER OF SEQUENCES: 32

CC ADDRESSEE: E. I du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.

```
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
```

CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:

CC REGISTRATION NUMBER: 33 692
CC REFERENCE/DOCKET NUMBER: BS-1036-P-
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 9:

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CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 404 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
SQ      SEQUENCE 404 AA; 46517 MW; 906055 CN
```

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 7.18; | Score 9; | DB 3; | Length 404; |
| Best Local Similarity | 100.08; | Pred. No. 7.47e-03; | | |
| Matches | 9; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

| | | | |
|----|-----|----------|-----|
| Db | 277 | VTYLNHGH | 285 |
| | | | |
| Qy | 118 | VTYLNHGH | 126 |

| | | | | |
|--------|-------------------|-----------|------|--------|
| RESULT | 8 | STANDARD; | PRT; | 435 AA |
| ID | PCT-US94-01321-12 | | | |

AC XXXXXX

| | |
|----|--|
| DE | Sequence 12, Application PC/TUS9401321 |
| XX | |
| CC | Sequence 12, Application PC/TUS9401321 |
| CC | GENERAL INFORMATION: |

CC TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
CC TITLE OF INVENTION: In Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321
CC FILING DATE: 04-FEB-1994

CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014433
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 12:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 435 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CQ SEQUENCE 435 AA; 50136 MW; 1054240 Cn

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 7.18; | Score 9; | DB 3; | Length 435; |
| Best Local Similarity | 100.08; | Pred. No. 7.47e-03; | | |
| Matches | 9; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0 |

| | | | |
|----|-----|----------|-----|
| Db | 312 | VTYLNHGH | 320 |
| | | | |
| QY | 118 | VTYLNHGH | 126 |

| | | | | | |
|--------|------------------|-----------|------|-----|----|
| RESULT | 9 | STANDARD: | PRT: | 446 | AA |
| ID | PCT-US92-10284-5 | | | | |

AC XXXXXXXX

| | |
|----|---------------------------------------|
| DE | Sequence 5, Application PC/TUS9210284 |
| XX | |
| CC | Sequence 5, Application PC/TUS921028 |

CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SO
Query Match 7.1%; Score 9; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.47e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 319 VTYLHHGH 327
QY 118 VTYLHHGH 126
RESULT 10
ID PCT-US94-01321-10 STANDARD; PRT: 446 AA.
XX xxxxxx
AC
DT
XX
DE Sequence 10, Application PC/TUS9401321
XX
CC Sequence 10, Application PC/TUS9401321
CC GENERAL INFORMATION:
CC APPLICANT:
CC TITLE OF INVENTION: Altered linolenic and linoleic Acid Content
CC TITLE OF INVENTION: in Plants
CC NUMBER OF SEQUENCES: 72
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US94/01321

CC FILING DATE: 04-FEB-1994
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/156551
CC FILING DATE: 22-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/014431
CC FILING DATE: 05-FEB-1993
CC INFORMATION FOR SEQ ID NO: 10:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 446 AA; 51174 MW; 1094717 CN;
SO
Query Match 7.1%; Score 9; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 7.47e-03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 319 VTYLHHGH 327
QY 118 VTYLHHGH 126
RESULT 11
ID PCT-US92-10284-17 STANDARD; PRT: 156 AA.
XX xxxxxx
AC
DT
XX
DE Sequence 17, Application PC/TUS9210284
XX
CC Sequence 17, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadev, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID

CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYDROPHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pcdx-2 and pycs07
CC SEQUENCE 156 AA: 17771 MW: 126823 CN:

| | | | | |
|-----------------------|---------|---------------------|--------|---------------|
| Query Match | 5.68; | Score 7; | DB 3; | Length 156; |
| Best Local Similarity | 100.0%; | Pred. No. 2.36e+00; | | |
| Matches | 7; | Conservative | 0; | Mismatches 0; |
| | | | Indels | 0; |
| | | | Gaps | 0; |

| | | | |
|----|-----|---------|---|
| Db | 147 | HHQNHGH | 1 |
| | | | |
| Qy | 1 | HHQNHGH | 7 |

RESULT 12
ID US-08-320-982-20 STANDARD; PRT; 24 AA
vv

Sequence 20, Application US/08320982

CC Sequence 20, Application US/08320982
CC Patent No. 5801026
CC CURRENT INFORMATION

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC NUMBER OF SEQUENCES: 48

CC ADDRESSEE: CUSHMAN DABY & CUSHMAN L.L.P
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.

```
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
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CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220

CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:

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CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 24 AA: 2877 MW: 3868 CN
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Query Match 4.88; Score 6; DB 2; Length 24;

| | |
|-------------------------------|------------------------------------|
| Best Local Similarity 100.0%; | Pred. NO. 3.40e+01; |
| Matches 6; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |

| | | | |
|----|-----|--------|-----|
| Db | 12 | FVWMLD | 17 |
| | | | |
| QY | 111 | FVWMLD | 116 |

| | | | |
|--------|------------------|-----------|-------------|
| RESULT | 13 | | |
| ID | US-08-320-982-14 | STANDARD; | PRT; 24 AA. |

Sequence 14, Application US/08320982

CC Sequence 14, Application US/08320982
CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA
CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:
CC

CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC

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CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: PatentIn Release #1.0, Version #1.25
CC      CURRENT APPLICATION DATA:
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CC APPLICATION NUMBER: US/08/320,983
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:

CC NAME: KOKULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 14
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 24 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single

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CC      TOPOLOGY: linear
CC      MOLECULE TYPE: peptide
SQ      SEQUENCE  24 AA; 2877 MW; 3868 CN;

Query Match      4.88;      SCORE 6;  DB 2; length 24;
Best Local Similarity 100.0%;      Pred. NO. 3.4e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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| Db | 12 | EVMWLD | 17 |
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| QY | 111 | EVMWLD | 116 |

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| QY | 111 | EVMWLD | 116 |

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| ID | US-08-314-596-20 |
| STANDARD: | PRT; 24 AA |

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DT
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Sequence 20, Application US/08314596
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Sequence 20, Application US/08314596
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Patent No. 5668292
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GENERAL INFORMATION:
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APPLICANT: SOMERVILLE, CHRIS
CC
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APPLICANT: VAN DE LOO, FRANK
CC
CC
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC
CC
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC
CC
NUMBER OF SEQUENCES: 48
CC
CC
CORRESPONDENCE ADDRESS:
CC
CC
ADDRESSEE: CUSHMAN DARB Y & CUSHMAN L.L.P.
CC
CC
STREET: 1100 NEW YORK AVENUE, N.W.
CC
CC
CITY: WASHINGTON
CC
CC
STATE: D.C.
CC
CC
COUNTRY: U.S.A.
CC
CC
ZIP: 20005
CC
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COMPUTER READABLE FORM:
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CC
MEDIUM TYPE: floppy disk
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CC
COMPUTER: IBM PC compatible
CC
CC
OPERATING SYSTEM: PC-DOS/MS-DOS
CC
CC
SOFTWARE: PatentIn Release #1.0, Version #1.25
CC
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CURRENT APPLICATION DATA:
CC
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APPLICATION NUMBER: US/08/314,596
CC
CC
FILING DATE: 26-SEP-1994
CC
CC
CLASSIFICATION: 435
CC
CC
ATTORNEY/AGENT INFORMATION:
CC
CC
NAME: KOKULIS, PAUL N.
CC
CC
REGISTRATION NUMBER: 16,773
CC
CC
REFERENCE/DOCKET NUMBER: 206905/1220
CC
CC
TELECOMMUNICATION INFORMATION:
CC
CC
TELEPHONE: 202-861-3000
CC
CC
TELEFAX: 202-822-0944
CC
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INFORMATION FOR SEQ ID NO: 20:
CC
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SEQUENCE CHARACTERISTICS:
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LENGTH: 24 amino acids
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TYPE: amino acid
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STRANDEDNESS: single
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TOPOLOGY: linear
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MOLECULE TYPE: peptide
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SEQUENCE 24 AA: 2877 MW: 3868 CN;
SQ
Query Match 4.8%; Score 6; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3,406+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 12 FVWMID 17
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RESULT 15
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AC xxxxxx
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DT
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Patent No. 5801026
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GENERAL INFORMATION:
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APPLICANT: SOMERVILLE, CHRIS
CC
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APPLICANT: VAN DE LOO, FRANK
CC
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TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC
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TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
CC
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NUMBER OF SEQUENCES: 48
CC
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CORRESPONDENCE ADDRESS:
CC
CC
ADDRESSEE: CUSHMAN DARB Y & CUSHMAN L.L.P.
CC

```

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CC STREET: 1100 NEW YORK AVENUE, N.W.
CC CITY: WASHINGTON
CC STATE: D.C.
CC COUNTRY: U.S.A.
CC ZIP: 20005
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: KORULIS, PAUL N.
CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000
CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 8:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: Single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 37 AA: 4430 MW: 9485 CN:

Query Match 4.8%; Score 6; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 3.40e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Db 25 FVWMWD 30
07 111 FVWMWD 116

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Search completed: Sat Aug 21 12:53:23 1999
Job time : 9 secs.

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NW
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S
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R
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H

(7M)

Release 3.1A John F. Collins, Biocomputing Research Unit.
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Distribution rights by Oxford Molecular Ltd

Msrch:lp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat Aug 21 12:15:18 1999; Maspar time 5.60 Seconds

Tabular output not generated. 808.158 Million cell updates/sec

Title: >US-09-219-935-5

Description: (1-446) from US09219935.pep

Perfect Score: 446

Sequence: 1 MANLVSECGIRPLRIYTT.....EVVYKADNLTGEVKVRAD 446

Scoring table: TABLE uniprottable

Gap 60

Searched: 106580 seqs, 10152877 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: <a-issued

1:5A_COMB 2:5B_COMB 3:PCY9_COMB 4:backfiles1

Statistics: Mean 2.796; Variance 0.701; scale 3.989

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description | Pred. No. |
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| 2 | 446 | 100.0 | 446 | 3 | PCT-US92-1 Sequence 5, Applicatio | 0.00e+00 |
| 3 | 103 | 23.1 | 478 | 3 | PCT-US92-1 Sequence 7, Applicatio | 2.72e-154 |
| 4 | 103 | 23.1 | 404 | 3 | PCT-US92-1 Sequence 9, Applicatio | 2.72e-154 |
| 5 | 43 | 9.6 | 435 | 3 | PCT-US94-0 Sequence 12, Applicati | 3.41e-54 |
| 6 | 36 | 8.1 | 453 | 3 | PCT-US92-1 Sequence 13, Applicati | 7.58e-43 |
| 7 | 31 | 7.0 | 156 | 3 | PCT-US92-1 Sequence 17, Applicati | 7.71e-35 |
| 8 | 28 | 6.3 | 383 | 3 | PCT-US94-0 Sequence 2, Applicatio | 4.36e-30 |
| 9 | 28 | 6.3 | 386 | 3 | PCT-US92-1 Sequence 2, Applicatio | 4.36e-30 |
| 10 | 27 | 6.1 | 380 | 3 | PCT-US92-1 Sequence 11, Applicatio | 1.63e-28 |
| 11 | 25 | 5.6 | 37 | 2 | US-08-320- Sequence 6, Applicatio | 2.19e-25 |
| 12 | 25 | 5.6 | 37 | 2 | US-08-320- Sequence 22, Applicati | 2.19e-25 |
| 13 | 25 | 5.6 | 37 | 1 | US-08-314- Sequence 6, Applicatio | 2.19e-25 |
| 14 | 25 | 5.6 | 37 | 1 | US-08-314- Sequence 22, Applicati | 2.19e-25 |
| 15 | 22 | 4.9 | 37 | 1 | US-08-314- Sequence 2, Applicatio | 2.19e-25 |
| 16 | 22 | 4.9 | 37 | 1 | US-08-314- Sequence 16, Applicati | 9.57e-21 |
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| 18 | 22 | 4.9 | 37 | 2 | US-08-320- Sequence 16, Applicati | 9.57e-21 |
| 19 | 18 | 4.0 | 40 | 2 | US-08-320- Sequence 10, Applicati | 1.09e-14 |
| 20 | 18 | 4.0 | 40 | 2 | US-08-320- Sequence 18, Applicati | 1.09e-14 |
| 21 | 18 | 4.0 | 40 | 1 | US-08-314- Sequence 10, Applicati | 1.09e-14 |
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| 24 | 12 | 2.7 | 37 | 1 | US-08-314- Sequence 8, Applicatio | 4.77e-06 |
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| 27 | 11 | 2.5 | 40 | 2 | US-08-320- Sequence 24, Applicati | 1.09e-04 |
| 28 | 11 | 2.5 | 40 | 2 | US-08-320- Sequence 4, Applicatio | 1.09e-04 |
| 29 | 11 | 2.5 | 40 | 1 | US-08-314- Sequence 4, Applicatio | 1.09e-04 |
| 30 | 11 | 2.5 | 40 | 1 | US-08-314- Sequence 24, Applicati | 1.09e-04 |
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| 32 | 9 | 2.0 | 126 | 3 | PCT-US92-1 Sequence 15, Applicati | 7.45e-02 |
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| 35 | 8 | 1.8 | 8 | 3 | PCT-US94-0 Sequence 63, Applicati | 7.55e-01 |
| 36 | 8 | 1.8 | 20 | 1 | US-08-607- Sequence 6, Applicatio | 7.55e-01 |
| 37 | 8 | 1.8 | 20 | 1 | US-08-399- Sequence 6, Applicatio | 7.55e-01 |
| 38 | 8 | 1.8 | 20 | 2 | US-08-605- Sequence 6, Applicatio | 7.55e-01 |
| 39 | 8 | 1.8 | 597 | 1 | US-08-607- Sequence 4, Applicatio | 7.55e-01 |
| 40 | 8 | 1.8 | 597 | 2 | US-08-961- Sequence 4, Applicatio | 7.55e-01 |
| 41 | 8 | 1.8 | 597 | 2 | US-08-605- Sequence 4, Applicatio | 7.55e-01 |
| 42 | 8 | 1.8 | 598 | 1 | US-08-607- Sequence 14, Applicati | 7.55e-01 |
| 43 | 8 | 1.8 | 598 | 2 | US-08-399- Sequence 14, Applicati | 7.55e-01 |
| 44 | 8 | 1.8 | 598 | 2 | US-08-605- Sequence 14, Applicati | 7.55e-01 |
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ALIGNMENTS

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| AC | xxxxxx | GENERAL INFORMATION: | | | |
| AC | | APPLICANT: | | | |
| CC | | TITLE OF INVENTION: Altered Linoleic and Linoleic Acid Content | | | |
| CC | | MEDIUM OF INVENTION: In Plants | | | |
| CC | | NUMBER OF SEQUENCES: 72 | | | |
| CC | | COMPUTER READABLE FORM: | | | |
| CC | | MEDIUM TYPE: Floppy disk | | | |
| CC | | COMPUTER: IBM PC compatible | | | |
| CC | | OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| CC | | SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) | | | |
| CC | | CURRENT APPLICATION DATA: | | | |
| CC | | APPLICATION NUMBER: PCT/US94/01321 | | | |
| CC | | FILING DATE: 04-FEB-1994 | | | |
| CC | | CLASSIFICATION: | | | |
| CC | | PRIOR APPLICATION DATA: | | | |
| CC | | APPLICATION NUMBER: US 08/156551 | | | |
| CC | | FILING DATE: 22-NOV-1993 | | | |
| CC | | PRIOR APPLICATION DATA: | | | |
| CC | | APPLICATION NUMBER: US 08/014431 | | | |
| CC | | FILING DATE: 05-FEB-1993 | | | |
| CC | | INFORMATION FOR SEQ ID NO: 10: | | | |
| CC | | SEQUENCE CHARACTERISTICS: | | | |
| CC | | LENGTH: 446 amino acids | | | |
| CC | | TYPE: amino acid | | | |
| CC | | TOPOLOGY: linear | | | |
| CC | | MOLECULE TYPE: protein | | | |
| CC | | SEQUENCE 446 AA; 51174 MW; 1094717 CN; | | | |
| CC | | Query Match 100.0%; Score 446; DB 3; Length 446; | | | |
| CC | | Best Local Similarity 100.0%; Pred. No. 0.00e+00; | | | |
| CC | | Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
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| Qy | 1 | MANLVSECGIRPLRIYTTPRSNFLSNKKFRPSLSSSSYKTSSSPLSGLSRDSGFTTR 60 | | | |
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Db 121 VVRDVAIVFALAGAAYLNNMIWPLYLWLAOGTFWALFVLGHDGSGSFSNDPKLSVY 180
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Db 241 MAAVFFYLMAVSPGKSGSHYHPDSDLFLPKERKDVLTSTACTMAAALLVCLNFTIGIQ 300
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Db 301 MLKLGIPYWINVMWLDVFTYLHHGHGHEDKLPMYRGKEMSYLRGGLTTLDRDYGILNNIH 360
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AC xxxxxx
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DE Sequence 5, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A. 33,692
CC REGISTRATION NUMBER: BB-1036-A
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC INFORMATION FOR SEQ ID NO: 5:
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CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 446 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 446 AA: 51174 MW: 1094717 CN:
Query Match 100.0%; Score 446; DB 3; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MANVLSVSCGIRPLPRITTPRSNPLSNKKFRSLSSSTKITSSPLSFLNSRDGFT 60
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QY 61 NMAVNSVPLTTPFEESPLEEDNKORFDPGAPPPFNADIRAAIPKHCWKNPKMSLSY 120
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QY 301 MLKLGIPYWINVMWLDVFTYLHHGHGHEDKLPMYRGKEMSYLRGGLTTLDRDYGILNNIH 360
Db 361 HDIGTHVHNLFPQIPHYHLVEATEAAKPVLGKYYREBPKSGPLDLHLETLAKSIKEDH 420
QY 361 HDIGTHVHNLFPQIPHYHLVEATEAAKPVLGKYYREBPKSGPLDLHLETLAKSIKEDH 420
Db 421 YVSDGEVYVYKADPNLYGKGVKVRAD 446
QY 421 YVSDGEVYVYKADPNLYGKGVKVRAD 446
RESULT 3
ID PCT-US92-10284-7 STANDARD: PRT: 378 AA.
AC xxxxxx
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DE Sequence 7, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC CITY: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
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CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US92/10284  
CC FILING DATE: 19921203  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 07/804,259  
CC FILING DATE: 4 DECEMBER 1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Floyd, Linda A.  
CC REGISTRATION NUMBER: 33,692  
CC REFERENCE/DOCKET NUMBER: BB-1036-A  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (302) 992-4929  
CC TELEFAX: (302) 892-7949  
CC TELEX: 835420  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 378 amino acids  
CC TYPE: AMINO ACID  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: protein  
CC SEQUENCE 378 AA; 43528 MW; 793455 CN;  
SQ  
  
Query Match 23.1%; Score 103; DB 3; Length 378;  
Best Local Similarity 100.0%; Pred.No. 2.72e-154;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
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GENERAL INFORMATION:  
CC APPLICANT: Browne, John, Kinney, Anthony J.,  
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,  
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis  
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes  
CC TITLE OF INVENTION: from plants  
CC NUMBER OF SEQUENCES: 32  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: E. I. du Pont de Nemours and Company  
CC STREET: 1007 Market Street  
CC City: Wilmington  
CC STATE: Delaware  
CC COUNTRY: U.S.A.  
CC ZIP: 19898  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: Macintosh  
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CC SOFTWARE: Microsoft Word, 4.0  
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CC FILING DATE: 19921203  
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CC APPLICATION NUMBER: 07/804,259  
CC FILING DATE: 4 DECEMBER 1991  
CC ATTORNEY/AGENT INFORMATION:
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| CC | | ME: Floyd, Linda A. |
| CC | | REGISTRATION NUMBER: 33,692 |
| CC | | REFERENCE/DOCKET NUMBER: BB-1036-A |
| CC | | TELECOMMUNICATION INFORMATION: |
| CC | | TELEPHONE: (302) 992-4929 |
| CC | | TELEFAX: (302) 892-7949 |
| CC | | TELEX: 835420 |
| CC | | INFORMATION FOR SEQ ID NO: 9: |
| CC | | SEQUENCE CHARACTERISTICS: |
| CC | | LENGTH: 404 amino acids |
| CC | | TYPE: AMINO ACID |
| CC | | TOPOLOGY: linear |
| CC | | MOLECULE TYPE: protein |
| SQ | SEQUENCE | 404 AA; 46617 MW; 906055 CN; |
| | | |
| Db | | Query Match 23.1%; Score 103; DB 3; Length 404; Best Local Similarity 100.0%; Pred. No. 2,72e-154; |
| Matches | 103; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| | | |
| Db | 265 | IPIYINWMLDFVYLHHGHGHEKLPYRGKEWSYLLNGGLTTDDRDYGLINNHHDIGTH 324 IPIYINWMLDFVYLHHGHGHEKLPYRGKEWSYLLNGGLTTDDRDYGLINNHHDIGTH 366 |
| Qy | 307 | IPIYINWMLDFVYLHHGHGHEKLPYRGKEWSYLLNGGLTTDDRDYGLINNHHDIGTH 366 VIHHLFQIPHYLVEATEAKPVLGYRPPDKSGPLPHLL 409 |
| Qy | 367 | VIHHLFQIPHYLVEATEAKPVLGYRPPDKSGPLPHLL 409 |
| | | |
| RESULT | 5 | |
| ID | PCT-US94-01321-12 | STANDARD; PRT: 435 AA. |
| XX | | |
| AC | xxxxxx | |
| DT | | |
| XX | | |
| DE | | Sequence 12, Application PC/TUS9401321 |
| XX | | |
| CC | | Sequence 12, Application PC/TUS9401321 |
| CC | | GENERAL INFORMATION: |
| CC | | APPLICANT: |
| CC | | TITLE OF INVENTION: Altered linolenic and linoleic Acid Content |
| CC | | TITLE OF INVENTION: in plants |
| CC | | NUMBER OF SEQUENCES: 72 |
| CC | | COMPUTER READABLE FORM: |
| CC | | MEDIUM TYPE: floppy disk |
| CC | | COMPUTER: IBM PC compatible |
| CC | | OPERATING SYSTEM: PC-DOS/MS-DOS |
| CC | | SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) |
| CC | | CURRENT APPLICATION DATA: |
| CC | | APPLICATION NUMBER: PCT/US94/01321 |
| CC | | FILING DATE: 04-FEB-1994 |
| CC | | CLASSIFICATION: |
| CC | | PRIOR APPLICATION DATA: |
| CC | | APPLICATION NUMBER: US 08/156551 |
| CC | | FILING DATE: 22-NOV-1993 |
| CC | | PRIOR APPLICATION DATA: |
| CC | | APPLICATION NUMBER: US 08/014431 |
| CC | | FILING DATE: 05-FEB-1993 |
| CC | | INFORMATION FOR SEQ ID NO: 12: |
| CC | | SEQUENCE CHARACTERISTICS: |
| CC | | LENGTH: 435 amino acids |
| CC | | TYPE: amino acid |
| CC | | TOPOLOGY: linear |
| CC | | MOLECULE TYPE: protein |
| SQ | SEQUENCE | 435 AA; 50136 MW; 1054240 CN; |
| | | |
| Db | | Query Match 9.6%; Score 43; DB 3; Length 435; Best Local Similarity 100.0%; Pred. No. 3.41e-54; |
| Matches | 43; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| | | |
| Db | 349 | INNHHDIGTIVHNHLPQIRPNHLYLVATEAKPVLYLKRYREP 391 INNHHDIGTIVHNHLPQIRPNHLYLVATEAKPVLYLKRYREP 398 |
| Yy | 356 | INNHHDIGTIVHNHLPQIRPNHLYLVATEAKPVLYLKRYREP 398 |

| | | | | |
|---------|---|-----------------------------------|------|---------|
| RESULT | 6 | STANDARD; | PRT; | 453 AA. |
| ID | PCT-US92-10284-13 | | | |
| XX | xxxxxx | | | |
| XX | | | | |
| DT | | | | |
| XX | Sequence 13, Application PC/TUS9210284 | | | |
| DE | | | | |
| XX | Sequence 13, Application PC/TUS9210284 | | | |
| CC | Sequence 13, Application PC/TUS9210284 | | | |
| CC | GENERAL INFORMATION: | | | |
| CC | APPLICANT: Browne, John, Kinney, Anthony J., | | | |
| CC | APPLICANT: Pierce, John, Wierzbicki, Anna M., | | | |
| CC | APPLICANT: Yadav, Narendra S., Perez-Grau, Luis | | | |
| CC | TITLE OF INVENTION: Fatty Acid Desaturase Genes | | | |
| CC | TITLE OF INVENTION: from plants | | | |
| CC | NUMBER OF SEQUENCES: 32 | | | |
| CC | CORRESPONDENCE ADDRESS: | | | |
| CC | ADDRESSEE: E. I. du Pont de Nemours and Company | | | |
| CC | STREET: 1007 Market Street | | | |
| CC | City: Wilmington | | | |
| CC | STATE: Delaware | | | |
| CC | COUNTRY: U.S.A. | | | |
| CC | ZIP: 19898 | | | |
| CC | COMPUTER READABLE FORM: | | | |
| CC | MEDIUM TYPE: Floppy disk | | | |
| CC | COMPUTER: Macintosh | | | |
| CC | OPERATING SYSTEM: Macintosh System, 6.0 | | | |
| CC | SOFTWARE: Microsoft Word, 4.0 | | | |
| CC | CURRENT APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: 9921023 | | | |
| CC | FILING DATE: 1992103 | | | |
| CC | CLASSIFICATION: 435 | | | |
| CC | PRIOR APPLICATION DATA: | | | |
| CC | APPLICATION NUMBER: 07/804,259 | | | |
| CC | FILING DATE: 4 DECEMBER 1991 | | | |
| CC | ATTORNEY/AGENT INFORMATION: | | | |
| CC | NAME: Floyd, Linda A. | | | |
| CC | REGISTRATION NUMBER: 33,692 | | | |
| CC | REFERENCE/DOCKET NUMBER: BB-1036-A | | | |
| CC | TELECOMMUNICATION INFORMATION: | | | |
| CC | TELEPHONE: (302) 992-4929 | | | |
| CC | TELEFAX: (302) 892-7949 | | | |
| CC | TELEX: 835420 | | | |
| CC | INFORMATION FOR SEQ ID NO: 13: | | | |
| CC | SEQUENCE CHARACTERISTICS: | | | |
| CC | LENGTH: 453 amino acids | | | |
| CC | TYPE: AMINO ACID | | | |
| CC | TOPOLOGY: linear | | | |
| CC | MOLECULE TYPE: protein | | | |
| CC | SEQUENCE 453 AA; 51362 MW; 1146882 CN; | | | |
| DB | Query Match | 8.1%; Score 36; DB 3; Length 453; | | |
| | Best Local Similarity 100.0%; Pred. No. 7,58e-43; | | | |
| Matches | 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| DB | 327 VTYLHHGHGDEKLPWYRGKEWSTYRGGLTTIDRDYG 362 | | | |
| | | | | |
| QY | 319 VTYLHHGHGDEKLPWYRGKEWSTYRGGLTTIDRDYG 354 | | | |
| RESULT | 7 | STANDARD; | PRT; | 156 AA. |
| ID | PCT-US92-10284-17 | | | |
| XX | xxxxxx | | | |
| XX | | | | |
| DT | | | | |
| XX | Sequence 17, Application PC/TUS9210284 | | | |
| DE | | | | |
| XX | Sequence 17, Application PC/TUS9210284 | | | |
| CC | | | | |

```

CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC City: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4925
CC TELEFAX: (302) 892-7949
CC
CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFad2-2 and pYacp7
CC
CC SEQUENCE 156 AA; 17771 MW; 126823 CN;
SQ
Query Match 7.0%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 7,71e-35;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 GHLHSSILVPIYHGWRISHRTHQNHGHVEN 156
OY 181 GHLHSSILVPIYHGWRISHRTHQNHGHVEN 211

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CC GENERAL INFORMATION:
CC APPLICANT: Browne, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC City: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4925
CC TELEFAX: (302) 892-7949
CC
CC CC INFORMATION FOR SEQ ID NO: 17:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 156 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: unknown
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: YES
CC FRAGMENT TYPE: N-terminal
CC ORIGINAL SOURCE:
CC ORGANISM: Arabidopsis thaliana
CC IMMEDIATE SOURCE:
CC CLONE: pFad2-2 and pYacp7
CC
CC SEQUENCE 156 AA; 17771 MW; 126823 CN;
SQ
Query Match 7.0%; Score 31; DB 3; Length 156;
Best Local Similarity 100.0%; Pred. No. 7,71e-35;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 126 GHLHSSILVPIYHGWRISHRTHQNHGVEN 156
OY 181 GHLHSSILVPIYHGWRISHRTHQNHGVEN 211

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| CC | | COMPUTER READABLE FORM: |
| CC | | MEDIUM TYPE: Floppy disk |
| CC | | COMPUTER: IBM PC compatible |
| CC | | OPERATING SYSTEM: PC-DOS/MS-DOS |
| CC | | SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) |
| CC | | CURRENT APPLICATION DATA: |
| CC | | APPLICATION NUMBER: PCT/US94/01121 |
| CC | | FILING DATE: 04-FEB-1994 |
| CC | | CLASSIFICATION: |
| CC | | PRIOR APPLICATION DATA: |
| CC | | APPLICATION NUMBER: US 08/156551 |
| CC | | FILING DATE: 22-NOV-1993 |
| CC | | PRIOR APPLICATION DATA: |
| CC | | APPLICATION NUMBER: US 08/014431 |
| CC | | FILING DATE: 05-FEB-1993 |
| CC | | INFORMATION FOR SEQ ID NO: 2: |
| CC | | SEQUENCE CHARACTERISTICS: |
| CC | | LENGTH: 383 amino acids |
| CC | | TYPE: amino acid |
| CC | | TOPOLOGY: linear |
| CC | | MOLECULE TYPE: protein |
| SQ | | SEQUENCE 383 AA; 43936 MW; 846574 CN; |
| Dn | | Query Match 6.3%; Score 28; DB 3; Length 383; |
| Oy | | Best Local Similarity 100.0%; Pred. No. 4.36e-30; |
| | | Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |
| Db | 123 | ILVPYHGWIRISHRTHQHNGHVNDSEW 150 |
| | | |
| Oy | 188 | ILVPYHGWIRISHRTHQHNGHVNDSEW 215 |
| RESULT | 9 | |
| ID | PCT-US92-10284-2 | STANDARD; PRT; 386 AA. |
| AC | xxxxxx | |
| XX | | |
| DT | | |
| XX | | |
| DE | | Sequence 2, Application PC/TUS9210284 |
| CC | | |
| CC | | GENERAL INFORMATION: |
| CC | | APPLICANT: Browne, John, Kinney, Anthony J., |
| CC | | APPLICANT: Pierce, John, Wierzbicki, Anna M., |
| CC | | APPLICANT: Yadav, Narendra S., Perez-Grau, Luis |
| CC | | TITLE OF INVENTION: Fatty Acid Desaturase Genes |
| CC | | TITLE OF INVENTION: from Plants |
| CC | | NUMBER OF SEQUENCES: 32 |
| CC | | CORRESPONDENCE ADDRESS: |
| CC | | ADDRESSEE: E. I. du Pont de Nemours and Company |
| CC | | STREET: 1007 Market Street |
| CC | | City: Wilmington |
| CC | | STATE: Delaware |
| CC | | COUNTRY: U.S.A. |
| CC | | ZIP: 19898 |
| CC | | COMPUTER READABLE FORM: |
| CC | | MEDIUM TYPE: Floppy disk |
| CC | | COMPUTER: Macintosh |
| CC | | OPERATING SYSTEM: Macintosh System, 6.0 |
| CC | | SOFTWARE: Microsoft Word, 4.0 |
| CC | | CURRENT APPLICATION DATA: |
| CC | | APPLICATION NUMBER: PCT/US92/10284 |
| CC | | FILING DATE: 19921203 |
| CC | | CLASSIFICATION: 435 |
| CC | | PRIOR APPLICATION DATA: |
| CC | | APPLICATION NUMBER: 07/804,259 |
| CC | | FILING DATE: 4 DECEMBER 1991 |
| CC | | ATTORNEY/AGENT INFORMATION: |
| CC | | NAME: Floyd, Linda A. |
| CC | | REGISTRATION NUMBER: 33,692 |
| CC | | REFERENCE/DOCKET NUMBER: BB-1036-A |
| CC | | TELECOMMUNICATION INFORMATION: |

```

CC      TELEPHONE: (302) 992-4929
CC      TELEFAX: (302) 892-7949
CC      TELEX: 835420
CC      INFORMATION FOR SEQ ID NO: 2:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 386 amino acids
CC      TYPE: AMINO ACID
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 386 AA; 44076 MW; 854247 CN;
SQ
Query Match          6.3%; Score 28; DB 3; Length 386;
Best Local Similarity 100.0%; Pred. NO. 4.36e-30;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
Db
126 ILVYHGWRISRTTHQNHGHVNDSEDM 153
|||||
188 ILVYHGWRISRTTHQNHGHVNDSEDM 215
OY
RESULT 10
ID PCT-US92-10284-11 STANDARD; PRT; 380 AA.
XX AC xxxxxx
XX DT
XX
XX
Sequence 11, Application PC/TUS9210284
DE
CC Sequence 11, Application PC/TUS9210284
CC GENERAL INFORMATION:
CC APPLICANT: Browae, John, Kinney, Anthony J.,
CC APPLICANT: Pierce, John, Wierzbicki, Anna M.,
CC APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
CC TITLE OF INVENTION: Fatty Acid Desaturase Genes
CC TITLE OF INVENTION: from Plants
CC NUMBER OF SEQUENCES: 32
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: E. I. du Pont de Nemours and Company
CC STREET: 1007 Market Street
CC City: Wilmington
CC STATE: Delaware
CC COUNTRY: U.S.A.
CC ZIP: 19898
CC
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: Macintosh
CC OPERATING SYSTEM: Macintosh System, 6.0
CC SOFTWARE: Microsoft Word, 4.0
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10284
CC FILING DATE: 19921203
CC CLASSIFICATION: 435
CC
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/804,259
CC FILING DATE: 4 DECEMBER 1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Floyd, Linda A.
CC REGISTRATION NUMBER: 33,692
CC REFERENCE/DOCKET NUMBER: BB-1036-A
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (302) 992-4929
CC TELEFAX: (302) 892-7949
CC TELEX: 835420
CC
CC INFORMATION FOR SEQ ID NO: 11:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 380 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 380 AA; 44185 MW; 827651 CN;
SQ
Query Match          6.1%; Score 27; DB 3; Length 380;

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Best Local Similarity 100.0%; Pred. No. 1.63e-28;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 295 NIHHDGTHVHHLFPQIPHVLVEAT 321
|||||
QY 358 NIHHDGTHVHHLFPQIPHVLVEAT 384

RESULT 11
ID US-08-320-982-6 STANDARD; PRT; 37 AA.

Sequence 6, Application US/08320982

CC Patent No. 5801026
CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK

CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.

CC CITY: WASHINGTON
CC STATE: D.C.

CC COUNTRY: U.S.A.
CC ZIP: 20005

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994

CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994

CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.

CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids

CC TYPE: amino acid
CC STRANDEDNESS: single

CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

CC SEQUENCE 37 AA: 4331 MW; 8403 CN;

Query Match 5.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.19e-25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHHDGTHVHHLFPQIPHVLVEAT 25
|||||

QY 360 HHHDGTHVHHLFPQIPHVLVEAT 384

RESULT 12
ID US-08-320-982-22 STANDARD; PRT; 37 AA.

AC xxxxxx

XX XX
DT DT
DE DE
XX XX

Sequence 22, Application US/08320982
Patent No. 5801026

CC GENERAL INFORMATION:

CC APPLICANT: SOMERVILLE, CHRIS
CC APPLICANT: VAN DE LOO, FRANK

CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA

CC NUMBER OF SEQUENCES: 48
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.
CC STREET: 1100 NEW YORK AVENUE, N.W.

CC CITY: WASHINGTON
CC STATE: D.C.

CC COUNTRY: U.S.A.
CC ZIP: 20005

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/320,982
CC FILING DATE: 11-OCT-1994

CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/314,596
CC FILING DATE: 26-SEP-1994

CC ATTORNEY/AGENT INFORMATION:
CC NAME: KOKULIS, PAUL N.

CC REGISTRATION NUMBER: 16,773
CC REFERENCE/DOCKET NUMBER: 206905/1220

CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 202-861-3000

CC TELEFAX: 202-822-0944
CC INFORMATION FOR SEQ ID NO: 22:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 37 amino acids

CC TYPE: amino acid
CC STRANDEDNESS: single

CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

CC SEQUENCE 37 AA: 4331 MW; 8403 CN;

Query Match 5.6%; Score 25; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.19e-25;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHHDGTHVHHLFPQIPHVLVEAT 25
|||||

QY 360 HHHDGTHVHHLFPQIPHVLVEAT 384

RESULT 13
ID US-08-314-596-6 STANDARD; PRT; 37 AA.

AC xxxxxx

Sequence 6, Application US/08314596
Patent No. 5668292

CC GENERAL INFORMATION:
CC APPLICANT: SOMERVILLE, CHRIS

CC APPLICANT: VAN DE LOO, FRANK
CC TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO

CC TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLA

CC MOLECULE TYPE: peptide
SQ SEQUENCE 37 AA; 4407 MM; 7119 CN;

Query Match 4.9%; Score 22; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.57e-21;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 HHDIGTHVHHLPQIPHYHLV 22
|||
QY 360 HHDIGTHVHHLPQIPHYHLV 381

Search completed: Sat Aug 21 12:15:30 1999
Job time : 12 secs.

APPLICANT: Heltemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael NMN
APPLICANT: Bettler Ph.D., Bernhard NMN
APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/718,575
FILING DATE: 19910813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TELEX: 9103330318
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: GLUR3
FEATURE:
NAME/KEY: CDS
LOCATION: 167..2833
US-07-718-575-5

Query Match 8.6%; Score 22; DB 1; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTCTCTC 89
DB 36 CTCCTCTCTCTCTCTCTCTC 57

RESULT 5
US-08-481-206-5
Sequence 5, Application US/08481206
Patent No. 5739291
GENERAL INFORMATION:
APPLICANT: Heltemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael NMN
APPLICANT: Bettler Ph.D., Bernhard NMN
APPLICANT: Jensen Ph.D., Jan E.
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
CITY: Los Angeles

STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,767
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TELEX: 9103330318
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: GLUR3
FEATURE:
NAME/KEY: CDS
LOCATION: 167..2833
US-08-481-206-5

Query Match 8.6%; Score 22; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTCTCTC 89
DB 36 CTCCTCTCTCTCTCTCTCTC 57

RESULT 6
US-08-253-155A-23/C
Sequence 23, Application US/08253155A
Patent No. 5691147
GENERAL INFORMATION:
APPLICANT: Gyuris, Jenio
APPLICANT: Diasteta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155A
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.
 REGISTRATION NUMBER: 36,709
 REFERENCE/DOCKET NUMBER: MI-028
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 329 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-253-155A-23

Query Match 8.2%; Score 21; DB 2; Length 329;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 63 AGAGACTCTCTCTCTCTCT 83
 Db 157 AGAGACTCTCTCTCTCTCT 137

RESULT 7
 US-08-848-252-3
 Sequence 3, Application US/08848252
 Patent No. 5804177
 GENERAL INFORMATION:
 APPLICANT: Humphries, Keith R.
 TITLE OF INVENTION: METHOD OF USING CD24 AS A CELL MARKER
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Bereskin & Parr
 STREET: 40 King Street West
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5H 3Y2
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/848,252
 FILING DATE: 29-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/538,052
 FILING DATE:
 APPLICATION NUMBER: US 08/151,672
 FILING DATE: 15-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: McDiarmid, Shona S.
 REGISTRATION NUMBER: P-38,798
 REFERENCE/DOCKET NUMBER: 3158-028
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 364-7311
 TELEFAX: (416) 361-1398
 TELEX: 06-23115
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1800 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ORIGINAL SOURCE: Mus musculus
 IMMEDIATE SOURCE:
 LIBRARY: Mouse

CLONE: M1/69-J1ld Heat-Stable Antigen
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 73..150
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 151..300
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 73..303
 US-08-848-252-3

Query Match 7.5%; Score 19; DB 3; Length 1800;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTCTCT 86
 Db 269 CTCCTCTCTCTCTCTCTCT 287

RESULT 8
 US-08-468-853-1
 Sequence 1, Application US/08468853
 Patent No. 5670362
 GENERAL INFORMATION:
 APPLICANT: van den BOOGAART, Paul
 APPLICANT: KOK, Jacobus Johannas
 APPLICANT: VERMEULEN, Arnoldus Nicolaas
 TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Akzo No. 5670362el Patent Department
 STREET: 1300 Pilecard Drive
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/468,853
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/310,357
 FILING DATE: 21-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/102,865
 FILING DATE: 06-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/604,075
 FILING DATE: 18-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 91.201.523.7
 FILING DATE: 18-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary E. Gormley
 REGISTRATION NUMBER: 34,409
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: (301) 258-5200
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1491 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA

FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Elmeria acerulina
INDIVIDUAL ISOLATE: Merozoites
IMMEDIATE SOURCE:
LIBRARY: Merozoites cdna lambda gt11
CLONE: Bam200
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1344
US-08-468-853-1

Query Match 7.1%; Score 18; DB 2; Length 1491;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 CTCCTCCGCGATGCTGT 120
DB 346 CTCCTCCGCGATGCTGT 363

RESULT 9
US-08-435-933-5
Sequence 5, Application US/08435933
Patent No. 5693492
GENERAL INFORMATION:
APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Paresa, Philip S.
APPLICANT: Liu, Ken K.
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John W. Wallen III
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: US
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,933
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, III John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-435-933-5

Query Match 7.1%; Score 18; DB 2; Length 3958;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 68 CTCCTCTCTCTCTCTTC 85
DB 11111111111111111111

DB 3307 CTCCTCTCTCTCTCTTC 3324

RESULT 10
US-08-473-096-1
Sequence 1, Application US/08473096
Patent No. 5693773
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect for Windows 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,096
FILING DATE: June 7, 1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 95,606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 monomers
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOETHERICAL: NO
ANTI-SENSE: YES
US-08-473-096-1

Query Match 7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 11
US-08-473-096-2
Sequence 2, Application US/08473096
Patent No. 5693773
GENERAL INFORMATION:
APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000

```

: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-2

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 12
US-08-473-096-3
: Sequence 3, Application US/08473096
: Patent No. 5693773
: GENERAL INFORMATION:
: APPLICANT: Kandimala, Ekambar R.
: TITLE OF INVENTION: Triplex-Forming Antisense
: TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
: TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 S. Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-4

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

TELEPHONE: (312)715-1000
TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 monomers
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHEITICAL: NO
ANTI-SENSE: YES
US-08-473-096-3

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 13
US-08-473-096-4
: Sequence 4, Application US/08473096
: Patent No. 5693773
: GENERAL INFORMATION:
: APPLICANT: Kandimala, Ekambar R.
: TITLE OF INVENTION: Triplex-Forming Antisense
: TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
: TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 S. Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-4

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33
```

```

: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-3

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33

RESULT 13
US-08-473-096-4
: Sequence 4, Application US/08473096
: Patent No. 5693773
: GENERAL INFORMATION:
: APPLICANT: Kandimala, Ekambar R.
: TITLE OF INVENTION: Triplex-Forming Antisense
: TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting
: TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Banner & Allegretti, Ltd.
: STREET: 10 S. Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect for Windows 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/473,096
: FILING DATE: June 7, 1995
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Greenfield, Michael S.
: REGISTRATION NUMBER: 37,142
: REFERENCE/DOCKET NUMBER: 95,606
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312)715-1000
: TELEFAX: (312)715-1234
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 43 monomers
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: HYPOTHEITICAL: NO
: ANTI-SENSE: YES
: US-08-473-096-4

Query Match      7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTTC 85
DB 16 CTCCTCTCTCTCTCTTC 33
```

Db 16 CTCCTCTCTCTCTCTC 33

RESULT 14

US-08-473-096-5
Sequence 5, Application US/08473096
Patent No. 5693773

GENERAL INFORMATION:

APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir

TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting

TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
TITLE OF INVENTION: and Pyrimidines

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 S. Wacker Drive, Suite 3000

CITY: Chicago
STATE: Illinois

COUNTRY: U.S.A.
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,096

FILING DATE: June 7, 1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.

REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 95,606

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000

TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 43 monomers

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
HYPOTHEICAL: NO

ANTI-SENSE: YES
US-08-473-096-5

Query Match 7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTC 85
Db 16 CTCCTCTCTCTCTCTC 33

RESULT 15

US-08-473-096-11
Sequence 11, Application US/08473096
Patent No. 5693773

GENERAL INFORMATION:

APPLICANT: Kandimala, Ekambar R.
APPLICANT: Agrawal, Sudhir

TITLE OF INVENTION: Triplex-Forming Antisense
TITLE OF INVENTION: Oligonucleotides Having Abasic Linkers Targeting

TITLE OF INVENTION: Nucleic Acids Comprising Mixed Sequences of Purines
TITLE OF INVENTION: and Pyrimidines

NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 S. Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect for Windows 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,096

FILING DATE: June 7, 1995
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.

REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 95,606

TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)715-1000

TELEFAX: (312)715-1234
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 43 monomers

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
HYPOTHEICAL: NO

ANTI-SENSE: YES
US-08-473-096-11

Query Match 7.1%; Score 18; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 CTCCTCTCTCTCTCTC 85
Db 16 CTCCTCTCTCTCTCTC 33

Search completed: August 22, 1999, 05:28:01
Job time: 3639 sec

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| | | | |
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| Db | 1081 | TTGGTGAGAGTTGGTGTCCCAAGTATTAGAAAGATCAATTACGTACGACGACACGTGTAT | 1140 |
| Qy | 1141 | ATTGTCCTTCAGACAGACAGATCCAGATCTCTACGATTTACGCTTCGACAAATCTTAAATC | 1200 |
| Db | 1141 | ATTGTCCTTCAGACAGACAGATCCAGATCTCTACGATTTACGCTTCGACAAATCTTAAATC | 1200 |
| Qy | 1201 | AATTAACTCTCATTTGTTTAGCTCTCTTTAGAGATTAACACAGCCACTTTTAAATTTTAA | 1260 |
| Db | 1201 | AATTAACTCTCATTTGTTTAGCTCTCTTTAGAGATTAACACAGCCACTTTTAAATTTTAA | 1260 |
| Qy | 1261 | TTTCTGTGTCTTTTAAAGTTAAAGTGAAGTACGTGTAACCTCTTTTCTTTCTTTTCTT | 1320 |
| Db | 1261 | TTTCTGTGTCTTTTAAAGTTAAAGTGAAGTACGTGTAACCTCTTTTCTTTCTTTTCTT | 1320 |
| Qy | 1321 | TATTAATGATTTACATTCGAAGGCGTAA | 1350 |
| Db | 1321 | TATTAATGATTTACATTCGAAGGCGTAA | 1350 |

```

1 RESULT 2
2 PCT-US92-10284-3
3 Sequence 3, Application PC/TUS9210284
4 GENERAL INFORMATION:
5 APPLICANT: Browne, John, Kinney, Anthony J.,
6 APPLICANT: Pierce, John, Wierzbicki, Anna M.,
7 APPLICANT: Yadav, Narendra S., Perez-Grau, Luis
8 TITLE OF INVENTION: Fatty Acid Desaturase Genes
9 NUMBER OF SEQUENCES: 32
10 CORRESPONDENCE ADDRESSES:
11 ADDRESSEE: E. I. du Pont de Nemours and Company
12 STREET: 1007 Market Street
13 CITY: Wilmington
14 STATE: Delaware
15 COUNTRY: U.S.A.
16 ZIP: 19898
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: Macintosh
20 OPERATING SYSTEM: Macintosh System, 6.0
21 SOFTWARE: Microsoft Word, 4.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: PCT/US92/10284
24 FILING DATE: 19921203
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: 07/804,259
28 FILING DATE: 4 DECEMBER 1991
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Floyd, Linda A.
31 REGISTRATION NUMBER: 33,692
32 REFERENCE/DOCKET NUMBER: BB-1036-A
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (302) 992-4929
35 TELEFAX: (302) 892-7949
36 TELEX: 835420
37 INFORMATION FOR SEQ ID NO: 3:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 255 base pairs
40 TYPE: NUCLEIC ACID
41 STRANDEDNESS: double
42 TOPOLOGY: linear
43 MOLECULE TYPE: DNA (genomic)
44 HYPOTHEICAL: NO
45 ORIGINAL SOURCE:
46 ORGANISM: Arabidopsis thaliana
47 IMMEDIATE SOURCE:
48 FEATURE:
49 NAME/KEY: exon
50 LOCATION: 68..255
51 PCT-US92-10284-3

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|---------------------------|--------|--------------------|-------|-------------|
| Query Match | 13.9% | Score 188; | DB 5; | Length 255; |
| Best Local Similarity | 100.0% | Pred. No. 5.5e+81; | | |
| Matches 188; Conservative | 0; | Mismatches | 0; | Indels 0; |
| | | | | Gaps 0; |

[illegible]

RESULT 3
PCT-US94-01321-1
; Sequence 1, Application PC/TUS9401321
; GENERAL INFORMATION.

APPLICANT:

;; TITLE OF INVENTION: Altered Linolenic and Linoleic Acid Content
;; TITLE OF INVENTION: in Plants

```

; NUMBER OF SEQUENCES: 72
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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;
COMPUEN: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
;
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; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: PCT/US94/01321
FILING DATE: 04-FEB-1994

CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/156551

;; FILING DATE: 22-NOV-2011
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/014431
FILING DATE: 05-FEB-1993

INFORMATION FOR SEQ ID NO: 1

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1353 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double

```

TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS
LOCATION: 87..1238

PCT-US94-01321-1

| | | | | |
|--------------------------|--------|--------------------|-----------|--------------|
| Query Match | 3.7% | Score 50; | DB 5; | Length 1353; |
| Best Local Similarity | 100.0% | Pred. No. 4.9e-15; | | |
| Matches 50; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0; |

Qy 1129 GACACGCGTGATATTGTCTCTACGAGACAGATCCAGATCCTACGTTTA 1178
 |||||
 Db 1161 GACACTGGTGATATTGTCTCTACGAGACAGATCCAGATCTCTACGTTTA 1210

RESULT 4
US-07-718-575-5
: Sequence 5, Application US/07718575
: Patent No. 5202257
: GENERAL INFORMATION:
: APPLICANT: Helmenann Ph.D., Stephen F.

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APPLICANT: Sliard, Jacques
APPLICANT: Emi, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Durocher, Francine
TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
City: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,002
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-002-19

Query Match 1.6%; Score 22; DB 2; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 TCTTTTCTTTCTTTCTTTT 1321
DB 316 TCTTTTCTTTCTTTCTTTT 337

RESULT 8
US-08-481-206-5
Sequence 5, Application US/08481206
Patent No. 5739291
GENERAL INFORMATION:

APPLICANT: Heinemann Ph.D., Stephen F.
APPLICANT: Boulter Ph.D., James R.
APPLICANT: Hollmann Ph.D., Michael NMN
APPLICANT: Bettler Ph.D., Bernhard NMN
TITLE OF INVENTION: GLUTAMATE RECEPTOR COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 So. Flower St., Suite 2000
City: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,206
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/013,767
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Reiter Ph.D., Stephen E.
REGISTRATION NUMBER: 31192
REFERENCE/DOCKET NUMBER: P31 8962
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
TELEX: 910330318
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: Glur3
FEATURE:
NAME/KEY: CDS
LOCATION: 167..2833
US-08-481-206-5

Query Match 1.6%; Score 22; DB 3; Length 3083;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTCCTCTCTCTCTCTCTCTC 22
DB 36 CTCCTCTCTCTCTCTCTCTC 57

RESULT 9
US-08-483-554B-19
Sequence 19, Application US/08483554B
Patent No. 5747282
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harsman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavliqian, Sean V.
APPLICANT: Wiseman, Roger W.

```

APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-554B-19

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Query Match      1.6%; Score 22; DB 3; Length 513;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|----|------|------------------------|------|
| Qy | 1300 | TCTTTTTTTTTTCTTTTTTTTT | 1321 |
| | | | |
| Db | 316 | TCTTTTTTTTTTCTTTTTTTTT | 337 |

RESULT 10
US-08-488-011B-19
Sequence 19, Application US/08488011B
Patent No. 5753441
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldfarb, David E.
APPLICANT: Mikl, Yoshio

```

1  APPLICANT: Swenson, Jeff
2  APPLICANT: Kamb, Alexander
3  APPLICANT: Harshtman, Keith D.
4  APPLICANT: Shattuck-Hildens, Donna M.
5  APPLICANT: Tavtligian, Sean V.
6  APPLICANT: Wiseman, Roger W.
7  APPLICANT: Futreal, P. Andrew
8  TITLE OF INVENTION: 17q-linked Breast and Ovarian Cancer
9  TITLE OF INVENTION: Susceptibility Gene
10 NUMBER OF SEQUENCES: 85
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
13 STREET: 1201 New York Avenue, N.W., Suite 1000
14 City: Washington
15 STATE: DC
16 COUNTRY: USA
17 ZIP: 20005
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS
23 SOFTWARE: PatentIn Release #1.0, Version #1.30
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER: US/08/488,011B
26 FILING DATE: 07-JUN-1995
27 CLASSIFICATION: 435
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/409,305
30 FILING DATE: 24-MAR-1995
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: US 08/348,824
33 FILING DATE: 29-NOV-1994
34 PRIOR APPLICATION DATA:
35 APPLICATION NUMBER: US 08/308,104
36 FILING DATE: 16-SEP-1994
37 PRIOR APPLICATION DATA:
38 APPLICATION NUMBER: US 08/300,266
39 FILING DATE: 02-SEP-1994
40 PRIOR APPLICATION DATA:
41 APPLICATION NUMBER: US 08/285,221
42 FILING DATE: 12-AUG-1994
43 ATTORNEY/AGENT INFORMATION:
44 NAME: Ihnen, Jeffrey L.
45 REGISTRATION NUMBER: 28,957
46 REFERENCE/DOCKET NUMBER: 24884-109347-09
47 TELECOMMUNICATION INFORMATION:
48 TELEPHONE: 202-962-4810
49 TELEFAX: 202-962-8300
50 INFORMATION FOR SEQ ID NO: 19:
51 SEQUENCE CHARACTERISTICS:
52 LENGTH: 513 base pairs
53 TYPE: nucleic acid
54 STRANDEDNESS: double
55 TOPOLOGY: linear
56 MOLECULE TYPE: DNA (genomic)
57 HYPOTHETICAL: NO
58 ANTI-SENSE: NO
59 ORIGINAL SOURCE:
60 ORGANISM: Homo sapiens
61
62 US-08-488-011B-19

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Query Match Similarity      1.6%  Score 22:  DB 3;  Length 513;
Best Local Similarity      100.0%  Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1300 | TCTTTTTTTTTTCTTTTTTTTT | 1321 |
| | | | |
| Db | 316 | TCTTTTTTTTTTCTTTTTTTTT | 337 |

RESULT 11
US-08-644-664B-31

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; Sequence 31, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denny Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: GENITOPE-00912
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..186
; US-08-644-664B-31

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Query Match 1.6%; Score 22; DB 3; Length 189;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1030 TTGGGAAGATCTACAGAAC 1051
DB 54 TTGGGAAGATCTACAGAAC 75

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RESULT 12
PCT-US95-10202-19
; Sequence 19, Application PC/TUS9510202
; GENERAL INFORMATION:
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Simard, Jacques
; APPLICANT: Emi, Mitsuru
; APPLICANT: Nakamura, Yusuke
; TITLE OF INVENTION: In Vivo Mutations and Polymorphisms
; TITLE OF INVENTION: In the 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/10202
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/409,305
; FILING DATE: 24-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/348,824
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08-308,104
; FILING DATE: 16-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/300,266
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,221
; FILING DATE: 12-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109347
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 513 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; PCT-US95-10202-19

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DB 316 TCTTTTCTTTCTTTTCTTTT 337

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; Sequence 19, Application PC/TUS9510203
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:

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ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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  FILING DATE:
  CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US
    FILING DATE: 07-JUN-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/409,305
    FILING DATE: 24-MAR-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/348,824
    FILING DATE: 29-NOV-1994
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    FILING DATE: 16-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/300,266
    FILING DATE: 02-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/289,221
    FILING DATE: 12-AUG-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Ihnen, Jeffrey L.
    REGISTRATION NUMBER: 28,957
    REFERENCE/DOCKET NUMBER: 24884-109347
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-962-4810
      TELEFAX: 202-962-8300
    INFORMATION FOR SEQ ID NO: 19:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 513 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
        MOLECULE TYPE: DNA (genomic)
        HYPOTHETICAL: NO
        ANTI-SENSE: NO
        ORIGINAL SOURCE:
          ORGANISM: Homo sapiens
PCT-US95-10203-19

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RESULT 14
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Sequence 19, Application PC/TUS9510220
GENERAL INFORMATION:
  APPLICANT: Skolnick, Mark H.
  APPLICANT: Goldgar, David E.
  APPLICANT: Miki, Yoshio
  APPLICANT: Swenson, Jeff
  APPLICANT: Kamb, Alexander
  APPLICANT: Harshman, Keith D.
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APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavligian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: Method for Diagnosing a
TITLE OF INVENTION: Predisposition for Breast and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
  STREET: 1201 New York Avenue, N.W., Suite 1000
  CITY: Washington
  STATE: DC
  COUNTRY: USA
  ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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  FILING DATE:
  CLASSIFICATION:
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    APPLICATION NUMBER: US
    FILING DATE: 07-JUN-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/409,305
    FILING DATE: 24-MAR-1995
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/348,824
    FILING DATE: 29-NOV-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08-308,104
    FILING DATE: 16-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/300,266
    FILING DATE: 02-SEP-1994
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/289,221
    FILING DATE: 12-AUG-1994
  ATTORNEY/AGENT INFORMATION:
    NAME: Ihnen, Jeffrey L.
    REGISTRATION NUMBER: 28,957
    REFERENCE/DOCKET NUMBER: 24884-109347
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 202-962-4810
      TELEFAX: 202-962-8300
    INFORMATION FOR SEQ ID NO: 19:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 513 base pairs
        TYPE: nucleic acid
        STRANDEDNESS: double
        TOPOLOGY: linear
        MOLECULE TYPE: DNA (genomic)
        HYPOTHETICAL: NO
        ANTI-SENSE: NO
        ORIGINAL SOURCE:
          ORGANISM: Homo sapiens
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RESULT 15
US-08-312-312A-1
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Search completed: August 22, 1999, 05:27:58
Job time: 3636 sec

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: Sequence 1, Application US/08312312A
: Patent No. 5550024
: GENERAL INFORMATION:
: APPLICANT: Rothschild, Max F.
: APPLICANT: Tuggle, Christopher K.
: APPLICANT: Jacobson, Carol D.
: APPLICANT: Mlleham, Alan J.
: APPLICANT: Plastow, Graham S.
: APPLICANT: Vaske, David A.
: TITLE OF INVENTION: Genetic Markers for Pig Litter Size
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
: STREET: 801 Grand Suite 3200
: CITY: Des Moines
: STATE: Iowa
: COUNTRY: United States
: ZIP: 50309
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/312,312A
: FILING DATE: 26-SEP-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/961,819
: FILING DATE: 19-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/687,708
: FILING DATE: 19-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Nebel, Heidi S.
: REGISTRATION NUMBER: 37,719
: REFERENCE/DOCKET NUMBER: BRDC-4
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 515-288-3667
: TELEFAX: 515-288-1338
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3460 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 303..304
: OTHER INFORMATION: /note= "Gap in DNA sequence of
: OTHER INFORMATION: undetermined length"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1197..1198
: OTHER INFORMATION: /note= "Gap in DNA sequence of
: OTHER INFORMATION: undetermined length"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 534..600
: US-08-312-312A-1

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Best Local Similarity 100.0%; Pred. No. 0.35;
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DB 3041 AACCTCTTTTCTCTCTTTT 3061

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